L Number	Hits	Search Text	DB	Time stamp
1	6	cory NEAR suzanne	USPAT;	2004/03/29 14:36
		-	US-PGPUB;	
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1			DERWENT	
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17	8	bcl-w.clm.	USPAT;	2004/03/29 14:40
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18	10	(US-5883229-\$ or US-5789201-\$).did. or	USPAT;	2004/03/29 14:40
_		(US-20020119943-\$ or	US-PGPUB;	
		US-20040014218-\$).did. or (WO-9735971-\$ or	EPO;	
		WO-9914321-\$ or WO-9913710-\$ or	DERWENT	
		WO-9115116-\$).did. or (WO-9913710-\$ or		
		US-20020119943-\$).did.		

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FILE 'MEDLINE, CANCERLIT, SCISEARCH, CAPLUS' ENTERED AT 14:42:01 ON 29
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            186 S L3 AND BCL?
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     ANSWER 3 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
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     1997:650444 CAPLUS
ΑN
DN
     127:327462
     A novel mammalian gene, bcl-w, belongs to the
TI
     bcl-2 family of apoptosis-controlling genes
     PCT Int. Appl., 85 pp.
     CODEN: PIXXD2
     Cory, Suzanne; Adams, Jerry McKee; Gibson, Leonie M.; Holmgreen,
ΙN
     Shaun P.
     Human and mouse cDNAs for bcl-2-related gene bcl-
AB
     w and the corresponding proteins are disclosed. The present
     invention is broadly directed to therapeutic mols. capable of inter alia
     modulating apoptosis in mammalian cells. The therapeutic mols. of the
     present invention encompass genetic sequences and chemical entities capable
     of regulating expression of bcl-w family and which
     promotes cell survival. The therapeutic mols. of the present invention
     may have further utility in delaying cell cycle entry. In addition, the
     present invention extends to chemical entities capable of modulating activity
     and function of the translation product of the bcl-w
     gene. The present invention also extends to the translation product of
     the bcl-w gene and its use in, for example, therapy,
     diagnosis, antibody generation and, as a screening tool for therapeutic
     mols. capable of modulating physiol. cell death or survival and/or
     modulating cell cycle entry. The bcl-w gene was
     mapped to human chromosome 14q11.2. Alternative splicing of the
     bcl-w gene transcript produced an mRNA for a bcl
     -w-rox chimera. The bcl-w gene was
     expressed in many cell types. Amongst the tissues surveyed, the level was
     highest in brain, colon and salivary gland. A survey of 50 mouse
     hemopoietic cell lines revealed that bcl-w expression
     was common in cells of several myeloid lineages, including macrophage,
     megakaryocyte, erythroid and mast cell lines, but rare in either B or \mathtt{T}
     lymphoid lines.
     PATENT NO.
                       KIND DATE
                                              APPLICATION NO. DATE
                                                                19970327
                       A1 19971002
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PΤ
     WO 9735971
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     ANSWER 8 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
1.7
     1999:215553 CAPLUS
ΑN
DN
     130:235990
     Animals carrying bcl-w mutations and their use in the
TΙ
     study of male infertility
SO
     PCT Int. Appl., 52 pp.
     CODEN: PIXXD2
     Cory, Suzanne; Adams, Jerry; Print, Cris; Gibson, Leonie;
IN
     Koentgen, Frank
     Transgenic mice carrying a disruption of the bcl-w
AB
     gene or of genes interacting with it and that fail to undergo productive
     spermatogenesis and are male infertile are described for use in studies of
     male fertility and of the biol. role of bcl-w. Such
     animals can be used to screen for therapeutic mols. including genetic
     sequences capable of inducing, enhancing or otherwise facilitating
     spermatogenesis in said animals as well as a model for mols. and genetic
     sequences which can induce infertility. The bcl-w
     gene was disrupted by insertional inactivation. Inactivation of
     bcl-w did not affect survival of fetal and neonatal mice
     and the mutation showed a near-normal Mendelian segregation.
     Hematopoiesis was unaffected by the mutation but the testes showed
     heterogeneous pathol. changes in the seminiferous tubules. Sertoli cells
     remained normal although low in number and Leydig cell were increased by 50%.
     Germ cell nos. declined steadily with as the stage of development
     advanced. The mutation did not affect androgen levels or androgen
     responses in other organs.
                      KIND DATE
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     ANSWER 1 OF 10
                         MEDLINE on STN
     96358615
                  MEDLINE
AN
     bcl-w, a novel member of the bcl-2 family,
TI
     promotes cell survival.
     Oncogene, (1996 Aug 15) 13 (4) 665-75.
SO
     Journal code: 8711562. ISSN: 0950-9232.
     Gibson L; Holmgreen S P; Huang D C; Bernard O; Copeland N G; Jenkins N A;
AU
     Sutherland G R; Baker E; Adams J M; Cory S
     The prototypic mammalian regulator of cell death is bcl-2, the
AB
     oncogene implicated in the development of human follicular lymphoma.
     Several homologues of bcl-2 are now known. Using a PCR-based
     strategy we cloned a novel member of this gene family, denoted bcl
     -\mathbf{w}. The gene, which is highly conserved between mouse and
     human, resides near the T-cell antigen receptor alpha gene within the
     central portion of mouse chromosome 14 and on human chromosome 14 at band
     q11. Enforced expression of bcl-w rendered lymphoid
     and myeloid cells refractory to several (but not all) cytotoxic
     conditions. Thus, like Bcl-2 and Bcl-x, the
     Bcl-w protein promotes cell survival, in contrast to
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other close homologues, Bax and Bak, which facilitate cell death. Comparison of the expected amino acid sequence of Bcl-w with that of these relatives helps to delineate residues likely to convey survival or anti-survival function. While expression of bcl-w was uncommon in B or T lymphoid cell lines, the mRNA was observed in almost all murine myeloid cell lines analysed and in a wide range of tissues. These findings suggest that bcl-w participates in the control of apoptosis in multiple cell types. Its functional similarity to bcl-2 also makes it an attractive candidate proto-oncogene.

- L7 ANSWER 4 OF 10 MEDLINE on STN
- AN 1998445387 MEDLINE
- TI Apoptosis regulator **bcl-w** is essential for spermatogenesis but appears otherwise redundant.
- Proceedings of the National Academy of Sciences of the United States of America, (1998 Oct 13) 95 (21) 12424-31.

 Journal code: 7505876. ISSN: 0027-8424.
- AU Print C G; Loveland K L; Gibson L; Meehan T; Stylianou A; Wreford N; de Kretser D; Metcalf D; Kontgen F; Adams J M; Cory S
- Proteins of the Bcl-2 family are important regulators of ΑB apoptosis in many tissues of the embryo and adult. The recently isolated bcl-w gene encodes a pro-survival member of the Bcl-2 family, which is widely expressed. To explore its physiological role, we have inactivated the bcl-w gene in the mouse by homologous recombination. Mice that lack Bcl- ${f w}$ were viable, healthy, and normal in appearance. Most tissues exhibited typical histology, and hematopoiesis was unaffected, presumably due to redundant function with other pro-survival family members. Although female reproductive function was normal, the males were infertile. The testes developed normally, and the initial, prepubertal wave of spermatogenesis was largely unaffected. The seminiferous tubules of adult males, however, were disorganized, contained numerous apoptotic cells, and produced no mature sperm. Both Sertoli cells and germ cells of all types were reduced in number, the most mature germ cells being the most severely depleted. The bcl-w-/- mouse provides a unique model of failed spermatogenesis in the adult that may be relevant to some cases of human male sterility.
- L7 ANSWER 7 OF 10 MEDLINE on STN
- AN 1999310955 MEDLINE
- TI Survival activity of Bcl-2 homologs Bcl-w and Al only partially correlates with their ability to bind pro-apoptotic family members.
- SO Cell death and differentiation, (1999 Jun) 6 (6) 525-32. Journal code: 9437445. ISSN: 1350-9047.
- AU Holmgreen S P; Huang D C; Adams J M; Cory S
- Certain Bcl-2 family members promote cell survival, whereas AB others promote apoptosis. To explore further how heterodimerization of opposing members affects survival activity, we have compared the abilities of the anti-apoptotic Bcl-w and Al to bind to the pro-apoptotic Bax, Bak, Bad and Bik and to protect cells from their cytotoxic action. Bcl-w co-immunoprecipitated from cell lysates with Bax, Bak, Bad and Bik, but Al bound only Bak and Bik. Mutation of Al at a highly conserved glycine within the BH1 domain prevented binding, but the comparable Bcl-w mutant still bound Bak, Bad and Bik, indicating that the glycine is not essential for all heterodimerization. Bcl-w and Al protected against apoptosis induced by over-expression of Bax or Bad but not that induced by Bak or Bik. With several gene pairs, binding and protection were discordant. The results may reflect critical threshold affinities but also suggest that certain pro-apoptotic proteins may also contribute to apoptosis by a mechanism independent of binding pro-survival proteins.
- L7 ANSWER 9 OF 10 MEDLINE on STN
- AN 2001360165 MEDLINE
- TI Tissue expression and subcellular localization of the pro-survival molecule Bcl-w.
- SO Cell death and differentiation, (2001 May) 8 (5) 486-94.

- Journal code: 9437445. ISSN: 1350-9047.
- AU O'Reilly L A; Print C; Hausmann G; Moriishi K; Cory S; Huang D C; Strasser A
- Anti-apoptotic members of the Bcl-2 family, such as Bcl AB $-\mathbf{w}$, maintain cell viability by preventing the activation of the cell death effectors, the caspases. Gene targeting experiments in mice have demonstrated that Bcl-w is required for spermatogenesis and for survival of damaged epithelial cells in the gut. Bcl-w is, however, dispensable for physiological cell death in other tissues. Here we report on the analysis of Bclw protein expression using a panel of novel monoclonal antibodies. Bcl-w is found in a diverse range of tissues including colon, brain and testes. A survey of transformed cell lines and purified hematopoietic cells demonstrated that Bcl-w is expressed in cells of myeloid, lymphoid and epithelial origin. Subcellular fractionation and confocal laser scanning microscopy demonstrated that ${\bf Bcl\text{-}w}$ protein is associated with intracellular membranes. The implications of these results are discussed in the context of the phenotype of Bcl-w-null mice and recent data that suggest that Bcl-w may play a role in colon carcinogenesis.

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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX022529	RESULT 1
apoptosis controlling genes Patent: EP 0932674-A 6 04-AUG-1999;	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of	Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.		unclassified.	unidentified	unidentified		AX022529.1 GI:10046125	AX022529	Sequence 6 from Patent EP0932674.	AX022529 583 bp DNA linear PAT 07-SEP-2000		

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/db_xref="G1:10046126"
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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                                                                              /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Score 583; DB 6; 1
Pred. No. 2.4e-121;
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TTGCTAGCAAGTGAA 583 TTGCTAGCAAGTGAA 583	GIGCIGACGGGGGCCGIGGCACIG 540	GACGGGGCCTGGAGGAGGCGCGG 480	CGGCTGGTCGACTGGATCCACAGC 420	AAGGAGATGGAACCACTGGTGGGA 360 	RGGGGCCGCCTTGTAGCCTTCTTT 300	GCTCAGCCCAGCAACGCTTCACC 240	TCGAGACCCGCTTCCGGCGCACC 180	CCGGGGAGGGCCCAGCAGCTGAC 120 	TGGTGGCAGACTTTGTAGGTTAT 60

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Adams, J.M.

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/mol_type="unassigned DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-JUN-1996) Molecular Biology Eliza Hall Institute of Medical Research, Hospital, Parkville, Victoria 3050, Austra
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/codon_start=1

/product="Bcl-w"

/protein_id="AAB09055.1"

/db_xref="GI:1572493"

/db_xref="GI:1572493"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGFGEGPAADFLHQ
AMRAAGDEFETRETSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNMGRLVAFFVF
GAALCAESVKKEMEPLVGQVQEMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
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Pred. No. 4.8e-120;
0; Mismatches 3;
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Gaps

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Matches
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Human |
D87461
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KIAA0271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:Chinainfoskazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 3542)
Ohara,O., Nagase,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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              AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
                                                                       ATGGCGACCCCAGCCTCGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGGTTAT
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                                                         ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
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                                                                                                                                                                                 /proteIn_id="BAA19666.1"
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/db_xref="G1:1944418"
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GAALCAESVNIKEMEPLVGQVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                  /cell_type="myloblast"
/tissue_type="brain"
/clone_lib="psporT 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HA6752"
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                                                                                                                                                                                                                                                                                               /gene="KIAA0271"
/note="similar to
                                                                                                                                                                                                                                                                                                                             /gene="KIAA0271"
177, .758
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                                                                                                                                                                                                                                                                                    (A24428)
                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
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                                                                                                                         98.6%;
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                                                                                                            Score 575; DB 9;
Pred. No. 1.2e-119;
0; Mismatches 5;
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AUTHORS
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AR020780
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Genes coding for bcl-y a bcl-2 homo

Genes Coding for bcl-y a bcl-2 homo

Patent: US 5789201-A 2 04-AUG-1998;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                             Similarity
                                                                               CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                                                     ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT
                                                                                                                                                                                       ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
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                        TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC
                                                          CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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/mol_type="unassigned
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Pred. No. 6.4e-118;
0; Mismatches 7;
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Rattus no
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Submitted (01-OCT-1998) Developmental
                                                                                                                                                                                                                                                                                                                                                                                                   Hamner, S., Skoglosa, Y. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hammer,S., Skoglosa,Y. and Lindholm,D. Differential expression of bcl-w and bcl-x developing and adult rat nervous system Neuroscience 91 (2), 673-684 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
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 /product="mac1-w"
/protein_id="mac64200.1"
/protein_id="mac64200.1"
/db xref="id1:3747130"
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AMRAAGDEFETERRTESDLAAQLHYTEGRAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMBEJVGQVQDWWYYLETRADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                       codon_
                                                                                                                                                        gene="bcl-w"
                                                                                                                                                                                          /gene="bcl-w"
                                                                                                                                                                                                                          tissue_type="brain"
dev_stage="postnatal"
                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                          note="Bcl-2
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(bcl-w)
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AY185100
2 (bases 1 to 1110)
Itoh,T., Itoh,A. and Pleasure,D.
Direct Submission
Submitted (21-NOV-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                       Itoh,T., Itoh,A. and Pleasure,D.
EG1-2-related protein family gene expression
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
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Mammalia; Eutheria;
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Rodentia;
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Pred. No. 7.7e-109;
0; Mismatches 34;
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SdC

/organism="Rattus

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                         Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                   Rattus norvegicus BCL-W
AY185098
AY185098.1 GI:32185280
                                                                         Rattus norvegicus (Norway
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/strain="Sprague-Dawley"
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BC1-2-related protein family gene exproliped differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
                                                                                                                                                                                                                                                                                                                                                      /codon_start=1/
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                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
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/mol_type="mRNA"
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, 3517 Civic Center
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                                                                   Bcl-w
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Pred. No. 8.5e-108;
0; Mismatches 35;
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Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-JUN-1996) Molecular Biology Uni-
Eliza Hall Institute of Medical Research, PO:
Hospital, Parkville, Victoria 3050, Australia
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibson, L., Holmgreen, S.P.,
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AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGGACGGGGCCCCTGGAGGAGGCGCGG
                                                                                            CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC
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/protein_id="AAB09056.1"
/protein_id="AAB09056.1"
/db_xref="G1:1572495"
/tamelation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
/translation="RATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETRERRTFSGLAAQLHVTVFGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
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/codon_start=1
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chromosome="14"
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Pred. No. 9.4e-108;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
AF030769
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                                           /note="mRNA destabilization 3428. .3441 /gene="Bcl-w"
                                                                                                                                                                                        /codon_start=1
/product="BCL-W"
/protein_id="AABB6430.1"
/protein_id="AABB6430.1"
/dbxref="Gi:2623250"
/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
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AMRAAGDEFETRFRRIFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAES\VIKEMEPLVGQVQDMMVAYLETRLADWIHSSGGWABFTALYGDGALEEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/10J"
/db_xref="taxon:10090"
/chromosome="14"
                                                                                                                                                                            RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                            179. .760
                                                                                            3356. .3364
/gene="Bcl-w"
                                                                                                                                                                                                                                                                                                         /gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                        'gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                         gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       map="19.5 cM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                            'gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                           number=3
                                                                                                                                                                                                                                                                                                                                                                                           number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                          number=1
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BCL-W (Bcl-w) mF
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89.7%;
 Score 522.8;
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mRNA,
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Atlanta, GA 30322, USA
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   10,
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                  REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ААССТСАССАСАВААССТТАТСТСТСТСОВАССТССССССССВССВСССАССАССТСАС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                           3473 bp mRNA
Mus musculus Bcl2-like protein 2 mRNA,
AY170344
      Submitted (22-SEP-2003) Biotechnology, Pingtung University, Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan Sequence update by submitter on Sep 22, 2003 this sequence version replaced gi:27497698.

Location/Qualifiers
1, 3473
                                                                                                                               Direct Submission
Submitted (29-OCT-2002) Biotechnology, 1
Hsueh Fu Road, Nei-Pu Hsiang, Pingtung,
3 (bases 1 to 3473)
                                                                                                      Direct Submission
                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                               Extraction from neonatal mouse
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                               (bases 1 to 3473)
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                                                                                                                                                                                                                                                                                                                                                 (house mouse)
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0; Mismatches
                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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, Taiwan 912, Taiwan
                                                                                                                                                    Pingtung University,
, Taiwan 912, Taiwan
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/protein id="AAO13177.2"
/db xref="G1:34857713"
/db xref="G1:34857713"
/translation="MATPASTPDTRALVAYFVGYQLRQKGYVCGAGPGEGPAADPLHQ
/translation="RTFRASTPDTRALVAYFVGYQLRQKGYVCGAGPGEGPAADPLHQ
AMRAAQDELQTRFRRTFSHLAAQLHVTPGSAQQRFTQYSDELFQGGPNWGRLVAFFVF
GAALCAESVNKHMEPLVGQVQDWMVAYLETRLAYWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFAYK"
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/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
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/dev_stage="neonatal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                       from
                                                                                            GI:10046127
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                                                                                                                                                   581 bp
Patent EP0932674.
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Pred. No. 5.9e-105;
0; Mismatches 45;
                                                                                                                                                                               DNA
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A novel mammalian gene, bol-w, belongs to
apoptosis-controlling genes
Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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A novel mammalian gene, bcl-w, belongs to the bcl-2 family
apoptosis-controlling genes
Patent: WO 9735971-A 8 02-0CT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZA
ADAMS JERRY MCKEE (AU); AMRAD OPERATIONS PTY LTD (AU)
; GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
Location/Qualifiers
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Search completed: March 29, 2004, 06:11:55 Job time: 2776.74 secs

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BG298789 602396527
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BU557210 AGENCOURT
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CCB79932 AMCNUUC: N
CB749817 AMCINUC: N
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BF204905 601866718
CB804140 AMCINUC: M
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B0646339 AGENCOURT
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PUBMED REFERENCE AUTHORS JOURNAL TITLE TITLE Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Adams, M.D. and Cargill, M. 2 (bases 1 to 582)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargili, M. Science 302 (5652), 1960-1963 (2003) gene trios 14671302 Inferring nonneutral evolution from human-chimp-mouse orthologous Submission 582 bp DNA linear GSS 17-DEC-, VIRTUAL TRANSCRIPT, partial sequence, GSS 17-DEC-2003

Result No.

Score

Match Length DB

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Description

SUMMARIES

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AY421020 Homo sapi AL157542 DKFZD761D BE793530 601590016 AY421022 Mus muscu

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 804)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemar
                                                                                                    AL157542 804 bp mRNA DKFZp761D0816 r1 761 (synonym: hamy2) Homo DKFZp761D0816 5', mRNA sequence.
AL157542 GI:7057943
                                                                          Homo sapiens
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/locus_tag="HCM7418"
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Pred. No. 1.5e-120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAIM
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This clone (DKFZp761D0816) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.
Location/Qualifiers
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Unpublished (1999)
Contact: MIPS
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                                                                                                                                                                                                                                       CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC
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                                       GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA
                                                        GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA
                                                                                               COTOTOCOGOGAACTOGOGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACT
                                                                                                                  | CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCGGGGCACTG
                                                                                                                                                        AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="btxTzp/sfl0816"
/tissue_type="advlt"
/dev_stage="advlt"
/lab_host="bH108"
/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.3%;
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Pred. No. 2.3e-115;
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BE793530.1 GI:10214832
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LICM800 row: p column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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CTCTTTGGGGCTGCACTGTGTGCTGAGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="small cell carcinoma"
cell_line="MGC3"
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     CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                       ATGGCGACCCCAGCCTCAACCCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT
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Query Match
Best Local Similarity
Matches 545; Conserv
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GSS.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Science 302 (5652), 1960-1963 (2003)
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Mus musculus BCL2L2 gene,
                                                                                                                                                                                                                                                                                                         Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-2003) Celera Genomics, 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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    Conservative
                                                                                                      /gene="BCL2L2"
/locus_tag="HCM7418"
                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                     organism="Mus musculus"
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                    89.7%;
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Score 522.8; DB 29;
Pred. No. 3.4e-109;
0; Mismatches 37;
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                                             Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Watsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                Genome Res.
20530913
11076861
                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashitzaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930488D08 product:Bcl2-like 2, full insert
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y full-length cDNA cloning
303, 19-44 (1999)
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Mara, A., Hayatsu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muzamatsu, M. and Hayashizaki, A., Yoshida, K., Yoshino, M., Muzamatsu, M. and Hayashizaki, T., The Therithire of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1949)
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/db_xref="MGI:1897773"
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                   20499374
11042159
                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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                     /tissue_type="lung"
/clone_lib="RIKEN full-length
/dev_stage="adult"
209._.790
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/mol_type="mRNA"
/strain="C57BL/6J"
  'note="unnamed protein
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                                                                                                          sex="male"
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db_xref="MGI:1896837"
                                                                                                                           clone="1200009L24"
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                                                                    mouse
                                                                    cDNA library"
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                                                                                                                               ACCESSION
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                                                                                                       cDNA clone .
BY715200
BY715200.1
                                                                                                                               BY715200 RIKEN full-length SY715200 RIKEN full-length CDNA clone 4930488D08 5', T
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 969)
                                                        Mus musculus
                                                                         Mus musculus
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/db_xref="G1:12836028"
/db_xref="G1:12836028"
/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
/translation="RATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETIFERTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASURTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative"
/codon_start=1
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                                                                                                          GI:27128317
                                                                       (house mouse)
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93.6%;
                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 7.6e-109;
D; Mismatches 37;
                                                                                                                                    πRNA linear EST 17-DEC-2002 meriched, adult male testis Mus musculus mRNA sequence.
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NSS Nikariot, Y., Purumo, M., Kashkawa, T., Adachi, J., Bono, H., Kondo, S., Kikariot, Y., Osato, M., Saito, R., Suruki, H., Yamanaka, T., Karaka, K., Karado, H., Yagi, K., Tomaruy, Hasegawa, Y., Nogami, A., Kikariot, H., Yagi, K., Tomaruy, Hasegawa, Y., Nogami, A., Kikariot, M., Guschenbush, J., Schrim, L.M., Kanabin, A., Matsuda, H., Hand, D.A., Quackenbush, J., Schrim, L.M., Kanabin, A., Matsuda, H., Batairo, S., Baite, K., Baike, J.A., Baatt, D., Brais, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fischer, C.F., Forrest, M., Partea, G., Batter, M., Kanadawa, Y., Keddieraki, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Keddieraki, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Keddieraki, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Keddieraki, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Keddieraki, R.M., King, B.L., Konagaya, A., Kawaji, H., Karahinani, J., Haris, A., Partea, G., Peocle, G., Riggald, M., Saltana, R., Osido, T., Pavan, M.J., Partea, G., Peocle, G., Riggald, M., Kandieraki, R.M., King, B.L., Konagaya, A., Kawaji, H., Kangawa, T., Radi, M., Sandaki, M., Sandaki, M., Schinekder, C., Semple, C.A., Setou, M., Shamaka, K., Sandaki, M., Sandaki,
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COMMENT

JOURNAL MEDLINE PUBMED

FEATURES

Location/Qualifiers

Bource

/organism="Mus musculus" /mol type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090"

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RESULT 8
BI770566
LOCUS
ACCESSION
                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="testis"
/dev_stage="adult"
/lab_host="SOLR"
/clone_lib="RIKEN ful
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93.58;
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                                     bp mRNA linear EST 25-SEP-20 sapiens cDNA clone IMAGE:5209862 5',
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMN1526 row: k column: 15
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
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                                     ACAAGTGCAGGAGTGGATGGTGGCCTACCT-GGAGACGCGGCTGGTCGACTGGATCCACA 418
                                                                                                                                                                                                              CAGGICTCCGACGAACTITTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
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    GTCTTTGGGGCTGCACTGTGTTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGG
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/clone libb"NIH_MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Corgan: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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Lab_host="DH108"
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Pred. No. 3.9e-100;
0; Mismatches 6;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)

Contact: "-""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nin.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMA10403 row: c column: 23
High quality sequence stop: 524.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/lab host="PH10B (phage-resistant)"
/lab host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC 94"
/note="Corgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 Mb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:10090"
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CR30109 y1 Human Retinal pigment (Un-normalized, unamplified): cs 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                  Email: graeme@helix.nih.gov
plate: 20 row: c column: 09
Seq primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
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Mol. Vis. 8 (4), 205-220 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 402 3452
Fax: 301 496 0078
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/clone_lib="Human Retinal pigment epithelium/choroid (Un-normalized, unamplified): cs" /note="Organ: Eye; Vector: pCMVSPORT6; Two different eyes (75-80 years old) yielded approximately 600 mg of the content of the co
                                                                                                                                     /tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                        /db xref="taxon:9606"
/clone="cs20c09"
                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
/mol_type="mRNA"
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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 643)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGTGCAGGAGTGGATGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC
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602111728F1 NCI_CGAP_Kid14 Mus n
5', mRNA sequence.
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EST.
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      Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     بو
                                                                                            Mus musculus (house mouse)
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/clone libe"NIH MGC 118"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV
/note="Vector: pcm, solution of the sector of the 
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/lab_host="DH108"
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/db_xref="taxon:9606"
/clone="IMAGE:5218294"
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Pred. No. 4.4e-85;
0; Mismatches 29;
         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Gaps

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60

REFERENCE AUTHORS TITLE JOURNAL COMMENT

IMAGE: 4239798 EST 12-JAN-2001

Mus

475

419

499

359

439 300 379

240 319 180 259 120

SOURCE ORGANISM

Homo sapiens (human)

ACCESSION VERSION

BI910270.1 mRNA sequence. BI910270

GI:16173653

KEYWORDS

RESULT 11 BI910270 LOCUS

DEFINITION

603069493F1 NIH_MGC_118

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595 421 Š 밁 Ş 밁 Ś 片

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Matches 446; Query Match

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Local Similarity

76.0%; 98.7%;

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355 181 295 121

JOURNAL COMMENT REFERENCE AUTHORS TITLE

FEATURES

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EST 03-APR-2003

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Query Match
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Lipublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM98953 row: h column: 07

High quality sequence star:: 3

High quality sequence stop: 650.

Location/Qualifiers

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/lab_host="DH10B (TI phage-resistant)"
/clone lib="NCI CGAP Kid14"
/clone lib="NCI CGAP Kid14"
/note="Organ: kīdney; Vector: pCMV-SPORT6; Site_1: Not /note="Organ: kīdney; Vector: pCMV-SPORT6; Site_1: Not /note= 2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"
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/strain="FVB/N"
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Pred. No. 2.6e-80;
0; Mismatches 40;
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AUTHORS
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Amgen Rat EST Program
Unpublished (2003)
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Mammalia; Eutheria;
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Plate: 00100 row: h column:
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/mol type="mrNA"
/db xref="taxon:10116"
/clone="nrdg1-00100-h10"
/tissue type="Dorsal Root Ganglia"
/clone Tib="nrdg1 (10855)"
/note="Vector: pSPORRY; Site_1: Sall; Site_2: Not1;
dorsal root ganglia"
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Submitted (10-UTL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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854 bp mRNA linear HTC 20-SEP-2003
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810435A13 product:Bc12-like 2, full insert
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
196. _.732
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AMRAAGDEFERRERETSDLAAQLHVTBGSAQORFTQVSDELFQGGPNMGRLVAFFVF
GBALCABSVNKEMBEDLVGQVQDMMVAYLETRLADWIHSSGGWVRSSQLLLSASLYKVG
LHGKIGPLMGGMGCAGRG"
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/db_xref="GI:12850488"
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/db_xref="MGI:1902183"
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/strain="C57BL/6J"
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SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
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Pred. No. 2.3e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein product; Bcl2-like
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BG298789
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Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 792)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG298789 792 bp mRNA linear EST 21-FEB-2001 602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5', mRNA_sequence.
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High quality sequence stop: 713.
Location/Qualifiers
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
                                                                                                                                                                                TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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                                                                                        CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                  TTCTCTGACCTGGC-GCTCAGCTACACGTGACCCCAGGCTCAGCCAGCAACGCTTCACC 337
                                                                                                                                                                                                                                                  CCGCTGCACCAAGCCATGCGGGGCTGCTGGAGACGAGTTTGAGACCCGGTTTCCGCCGCACC 278
                                                    CAGGITTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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/mb_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="MMAGE:4511215"
/clone="MMAGE:4511215"
/tissue_type="retina"
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/lab_host="PH103 (phage-resistant)"
/lone lib="NIH MGC 94"
/clone lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Sciurognathi; Muridae; Murinae; Mus.
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398 GTCTTTGGGGCTGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAAGCCTTTGGTGGGA 457

Qy 361 CAAGTGCAGGAGTGGATGGTGCCTACCTGGAGACTCGATCCACAGC 420

Db 458 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGATCCACAGC 517

Qy 421 AGTGGGGGCTGGCGA 437

Db 518 AGTGGGGGCTGGTAAGA 534
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Search completed: March 29, 2004, 07:28:08 Job time: 2302.9 secs

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Minimum DB
Maximum DB
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Maximum Match 10
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RESULT 1 AAT96577 ID AAT9 XX AAT9 XX AAT9 XX Huma XX Huma XX Huma XX Homo XX Clai XX C Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; ss. AAT96577 standard; DNA; 583 BP Homo sapiens Human bcl-w DNA. 22-APR-1998 (first entry) AAT96577; Location/Qualifiers

ALIGNMENTS

27-MAR-1996; 27-MAR-1997; 02-OCT-1997. WO9735971-A1. (AMRA-) AMRAD OPERATIONS PTY LTD. 96AU-00008965: 97WO-AU000199. /product= "bcl-w"

cory s, Adams JM, Gibson LM, Holmgreen

WPI; 1997-489635/45. P-PSDB; AAW36047.

diseases. Nucleic acid encoding apoptosis related gene bcl- \mathtt{w} - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative

Claim 3; Page 48; 86pp; English.

This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human

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The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival comember of the Bcl-2 family which is widely expressed and which is cessential for spermatogenesis. The invention relates generally to a comethod of treatment and to an animal model for the identification of comethod of treatment and to an animal model for the identification of complex and genetic sequences useful for inducing or reducing fertility. CC of male animals. Methods are provided for the treatment of infertility. CC or for reducing fertility, by modulating spermatogenesis. An animal model courries a mutation is at least one allele of the human or murine bcl-w carries a mutation is at least one allele of the human or murine bcl-w complex contributes and are substantially infertile, but possess no other complex tubules and are substantially infertile, but possess no other complex contributes as determined by histological examination. They can complex contributes and complex contributes including genetic sequences compable of inducing, enhancing or otherwise facilitating spermatogenesis compable, or which can induce infertility
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Query Match Best Local S Matches 583 Sequence 583 Similarity BP; 105 A; 157 C; 100.0%; Score 583; DB 2; I Pred. No. 7.3e-136; ; Mismatches 0; 210 G; 111 T; 0 U; Length 0 Other;

481 361 361 301 301 241 241 181 181 121 421 421 121 61 61 Н CAAGTGCAGGACTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC crcrrrecectecacrererereacidada dictal calcada de calcada de calcada de contra de contr CTCTTTGGGGCTGCACTGTGTGCTGAGAGATGTCAACAAGGAGATGGAACCACTGGTGGGA CAGGTCTCCGACGACCTTTTTCAAGGGGGCCCCAACTGGGGGCCGCCTTGTAGCCTTCTTT TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCACCCAGCAACGCTTCACC ccecrecaccaaeccareceeccaecrecaeareaerrecaeerreceaeaecceerreceeccaec CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCCCTTCCGGCGCACC AGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGGCCCAGCAGCTGAC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAAGGGCCCAGCAGCTGAC ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGACGCGG CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCCAAC CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC AGTGGGGGCTGGGGCGGAGTTCACAGCTCTATACGGGGGACGGGGGCCCTGGAGGAGGCGCGG 120 120 60 360 300 300 240 240 180 180 540 480 480 420 420 360

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Best Local Similarity
Matches 579; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2001; 2001DE-01000586.
26-CCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 582 BP;
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protozoacide;
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SULT 4 Z35729 ABZ35729 standard; DNA; 582 BP.

C ABZ35729;

07-FEB-2003 (first entry)

Human bcl-w polynucleotide SEQ ID NO 37.

Double stranded RNA; dsRNA; RNA; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.

Homo sapiens.

DE10100588-A1.

18-JUL-2002.

09-JAN-2001; 2001DE-01000588.

R 09~JAN-2001; 2001DE-01000588

A (RIBO-) RIBOPHARMA AG.

Kreutzer R, Limmer S, Rost S, Hadwiger P;

DR WPI; 2002-683450/74.

Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target.

Claim 13; Page 30-31; 100pp; German.

The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonuclectides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The

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                                                           Oligoribonucleotide; interferon; oncogene; cytokine; prion; inhibition; human; ds.
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This invention describes a novel method for inhibiting expression of a CC target gene by introducing into the cell that contains the target gene at CC least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at CC least a segment of one strand of the ds structure is complementary with CC the target gene and the cells are treated with interferon before CC introduction of dsRNAI. The method is used to inhibit expression of CC target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, developmental or prion genes, or invitues or viroids CC (pathogenic organisms (particularly plasmodia) or in viruses or viroids CC (pathogenic in humans, animals or plants). Treating the cells with CC interferon greatly increases the extent to which dsRNA can inhibit CC expression of the target genes, and the effect is even greater when dsRNA care modified to increase their stability. ABX09936-ABX10075 represent
                                                                                                                                                                                                                                                                                                                                                                                        introduction of the
                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting expression of target genes, e.g. oncogenes, in cells, b introduction of complementary double-stranded oligoribonucleotide, treating the cell with interferon.
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 35-36; 98pp; German.
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S Matches Query Match Best Local S Sequence 582 579; Similarity Conservative BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other, 99.0%; 0 Score 577.2; DB Pred. No. 2e-134; 0; Mismatches <u>د.</u> 9 Length Indels 0 Gaps 60 0

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Best Local S
Matches 579
                                                                                                                                                                                     The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonuclectide that has a double-gtranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration
                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                Sequence
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ilarity 99.5%;
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Anti-tumour; DNAzyme; bcl-2 gene; tumour; malignant; chemotherapy; radiation therapy; catalytic domain; enzyme; human; ds.

Homo sapiens

WO200299090-A1

07-JUN-2002; 2002WO-AU000739

07-JUN-2001; 2001AU-00005527

(JOHJ) JOHNSON & JOHNSON RES ALd LTD.

Ļ RJ, Saravolac EG, Dass

WPI; 2003-140617/13.

Novel DNAzyme useful for treating tumors, and for enhancing the sensitivity of malignant or virus infected cells to therapy, concatalytic domain and binding domain contiguous to the catalytic comprises domain.

Disclosure; Page 44-45; 67pp; English

The invention relates to a DNAzyme which specifically cleaves mRNA transcribed from a member of the bol-2 gene family. The DNAzymes compi a catalytic domain, binding domains contiguous with the 5' and 3' end the catalytic domain, and therefore hybridise with, the two regions immediately flanking the purine residue of the cleavage site within the comprise end of the

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                                                       Spermatogenesis; animal model; ss
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The present sequence is the human bcl-w gene encoding Bcl-w protein (see CC AAY05530), a pro-survival member of the Bcl-2 family which is widely CC expressed and which is essential for spermatogenesis. The invention CC relates generally to a method of treatment and to an animal model for the CC identification of molecules and genetic sequences useful for inducing or CC reducing ferrility, of male animals. Methods are provided for the CC treatment of infertility, or for reducing ferrility, by modulating CC spermatogenesis. An animal model carries a mutation is at least one CC allele of the human or murine bcl-w gene or in a gene associated with bcl CC substantially infertile, but possess no other major abnormalities as CC determined by histological examination. They can be used to screen for CC therapeutic molecules including genetic sequences capable of inducing, CC canancing or otherwise facilitating spermatogenesis in animals, or which CC can induce infertility
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Query Match Best Local Sim Matches 576; Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other: Similarity 98.3%; Score 573; DB 2; Pred. No. 2.3e-133; 0; Mismatches 5; Length 581 0

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                                                                                                                                                                                                                                                                                                                                                                family, components in the cell death pathway. The bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity, bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g.
                                                                                                                                                                                                                                                                                                                Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;
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                                                                                                                                       ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
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/product= "bcl-y"
/note= "No stop codon given"
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                                                                                                                                                                                                      Score 567.8; DB 2; Pred. No. 4.5e-132; D; Mismatches 7;
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RESULT 10
AAX15946
ID AAX15946
ID AAX15946
AC AAX15
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                                                                                                              WPI; 1999-214150/18
P-PSDB; AAW97392.
                                                                                                                                                                                                                                                                                                               23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-1997;
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97US-00798897.
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Novel bcl-y homologues of the rat and human bcl-2 protein - useful modulating programmed cell death.

for

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The present sequence encodes human bcl-y protein (Hbcl-y). The constitution also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-cy are homologues of the bcl-2 protein thought to be involved in corporation and encodes and necrosis. Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of complete the cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y could be used to treat conditions associated with a disruption of complete the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, considered the cell death and muscular degenerative diseases. Complete the spinal cord injuries and amyotrophic lateral sclerosis could death, aging, spinal cord injuries and amyotrophic lateral sclerosis conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this complete the conditions associated with prolonged cell lifes which remain viable in culture for an extended complete the conditions associated with prolonged cell conditions associated with prolonged cell conditions associated with prolonged cell cand auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites
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Best Local S
Matches 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
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GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG
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                                                                                                          CGTCTGCGGGAGGGGAACTGGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG
                                                                                                                                                                                                               AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCTGGAGGAGGAGGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                     GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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98.8%;
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Pred. No. 4.5e-132;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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RESULT 11 ADB52996

ADB52996 standard;

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ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT

Query Match Best Local S Matches 548

Local Similarity nes 548; Conserv

Conservative

0,

34; 9;

0;

Gaps

Length Indels

90.5%;

Score 527.6; DB Pred. No. 5e-122; 0; Mismatches 3

AXU

ADB52996;

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10-APR-2002;
10-APR-2002;
11-APR-2002;
19-APR-2002;
19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2002;
13-MAR-2002;
08-APR-2002;
10-APR-2002;
                                                 The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for the predict the toxic effects of a compound or an agent. These
                                                                                                                                                                                                                                                                                                                                                                            Mendrick
Elashoff
                                                                                                                                                                                                                                                                        Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
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04-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening;
                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-731472/69.
Sequence
                   screening. The present sequence represent modelling related gene sequence
                                                                                                                                                                                                                                              44; SEQ ID NO 3538; 874pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        GENE
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582
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2002US-0394230P.
2002US-0394253P.
2002US-0407668P.
2002US-0442900P.
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; 2002US-0378370P.
; 2002US-0378652P.
; 2002US-0378653P.
BP;
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2002US-0373602P.
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2002US-0371413P.
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                            The present sequence represents a primary ing related gene sequence from the present
111
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A; 157
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G; 114 T; 0 U; 0 Other;
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                                            rat hepatocyte
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RESULT 12
AAV28333
ID AAV28
XX AAV28
XX AAV28
XX CAAT COC
DE Rat L
XX SS; L
XX SS; L
XX SS; L
XX COS
PT CDS
FT CDS
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WPI; 1998-446079/38.
P-PSDB; AAW61391.
                                                                  Guastella
                                                                                                                                                                                              11-FEB-1997;
                                                                                                                                                                                                                                        04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; bcl-y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1998
                                                                                                                                                    23-FEB-1996;
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                                                                <u>د</u>
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                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .579
                                                                                                          INC
                                                                                                                                                                                                                                                                                                                 /product= "bcl-y"
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA;
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Best Local Similarity
Matches 544; Conserv
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                      cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 579 BP; 111 A; 157
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                                                                                                                                                    standard;
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                      the
                      rat bcl-y
                                                                                                                                                    cDNA;
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                      protein
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Pred. No. 7e-121;
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                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 13-16; 26pp; English
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11-FEB-1997;
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                         | CCGCTGCACCCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
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Pred. No. 7e-121;
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                                                                                                                                                                                                                                                                                               DB 2;
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16-SEP-1997;

97AU-00009228

HALL INST

MEDICAL RES

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WPI; 1999-243890/20

AAY05531

An animal model exhibiting reduced protein associated with Bcl-w.

levels

e E መ Bcl-w

protein and/or

(see

34;

52pp;

The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing,

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Spermatogenesis; animal model; ss
                                                                                                                                                                         Mouse bcl-w
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16-SEP-1998;
                               25-MAR-1999.
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                                                                                                                                               Bcl-2;
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Holmgreen
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This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w modulators, diagnosis, antibody production or screening of potential

G; 117 T; 0 **U;** 0 Other;

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STRAIN-Sprague-Dawley;
MEDLINE=22672518; PubMed=12787069;
Itch T., Itch A., Pleasure D.;
"Bcl-2-related protein family gene edifferentiation.";
J. Neurochem. 85:1500-1512 (2003).
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Q7TS60;
01-OCT-2003
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SMART; SM
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SEQUENCE
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                Local Similarity
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SM00265; BH4;
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; PS01080; BH1; 1.
; PS01258; BH2; 1.
; PS01260; BH4 1; 1.
; PS01260; BH4 2; 1.
; PS50063; BH4 2; 1.
; PS50063; BH4 2; 1.
                                                                                                                                                       MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                    GALVIVGAFFASK 193
                                                                 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                      FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                      MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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nilarity 98.4%;
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                                                                                                                                                                                                                                  219 AA;
                                                                                                                                                                                    Conservative
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Pred. No. 1.7e-80;
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Pred. No. 1.4e-80;
1; Mismatches 2
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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RESULT
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Matches 184
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MGD; MGI:108052; Red1212.
GO; GO:00016329; F:apoptosis regulator ac
GO; GO:0006915; P:apoptosis; IEA.

InterPro; IPR000712; BC12 BH.

InterPro; IPR003093; BC12 BH4.

InterPro; IPR003193; BC12 BH4.

InterPro; IPR003193; BC12 Family.
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SMART; SM00265; BH4; 1.

PROSITE; PS50062; BCL2: F

PROSITE; PS01080; BH1; 1

PROSITE; PS01258; BH2; 1
                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                          Q9CYW5;
Q9CYW5;
01-JUN-2001
01-JUN-2001
01-JUN-2003
Bcl2-like 2.
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Q8CGL4;
01-MAR-2003
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                     BCL2L2
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL; TISSUE=Skin;
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                                                                                                                                  Chordata;
Rodentia;
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Pred. No. 5.1e-77;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y.,
RA Aizawa K., Izawa M., Nishi K., Xiyosawa H., Xondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Xiyosawa H., Xondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinccha S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincha S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Heysashizaki Y.,
Hayashizaki Y.,
Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 400:685-690(2001).

EMBL; AKO13244; BAB28740.1; -.

RISSP; Q07817; IMAZ.

GG; GO:0016329; F:apoptosis; regulator activity; IEA

GG; GO:0006915; P:apoptosis; IEA.

RINterPro; IPR003093; Bc12_BH.

RINterPro; IPR003093; Bc12_BH4.

RINterPro; IPR003093; Bc12_Family.

R Pfam; PF00452; Bc12_Family.

R Pfam; PF00452; Bc12_Family:

R PF005ITE; PS01060; BH4; 1.

R PROSITE; PS01060; BH4; 1.
                                                                                                                                                                        Q8CFR2;
Q8CFR2;
01-MAR-2003
01-MAR-2003
01-OCT-2003
BC12-like 2.
                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
SEQUENCE FROM N.A. TISSUE=Eye;
Strausberg R.;
                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                           BCL2L2
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                                                                                                Chordata;
Rodentia;
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95.38;
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                                                                                                                                                                                            Last sequence update)
Last annotation updat
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Pred. No. 9.6e-60;
2; Mismatches 5;
                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                      178
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Best Local :
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InterPro; IPR003093; Bcl2_EH4.
InterPro; IPR003093; Bcl2_Em4.
InterPro; IPR002475; BcL2_family.
Pfam; PF00452; Bcl2_2; 1.
Pfam; PF02180; BH4; 1.
SNART; SN00265; Bcl2_FAMILY; 1.
SNART; SN00265; BH4; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH4; 1.
SEQUENCE 178 AA; 19119 MW; E2C
                                                                                                                                                                                                                                                                        EMBL; AY005131; AAF88137.1; -.
HSSP; P53563; 1AF3.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator ac
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR003012; BC12_BH4.
InterPro; IPR003099; BC12_BT4.
InterPro; IPR003099; BC12_Family.
InterPro; IPR003099; BC12_Family.
InterPro; IPR003099; BC12_Teg.
Pfam; PF00452; BC12_Teg.
Pfam; PF00450; BC12_Teg.
PROSITE; PS50062; BCL2 FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS50063; BH4 2; 1.
SEQUENCE 233 AA; 25986 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000
01-OCT-2000
01-JUN-2003
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Q9MYW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knott J.C., Robertson L., James E.R.;
"Rabbit Bcl-X.";
Submitted (JUL-2000) to the EMBL/GenB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                             SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
TIGRFAM6; TIGR00865; bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC040369; AAH40369.1; -.
MGD; MGI:108052; Bc1212.
GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up)
(TrEMBLrel. 24, Last annotation
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95.3%;
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Pred. No. 9.6e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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     12F0F30344D53F93 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity; IEA
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                                                                  Query Match
Best Local S
Matches 94
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                 MGD; MGI:88139; BC121.
GO; GO:0016320; C:membrane; IEA.
GO; GO:0016320; F:apoptosis regulator ac
GO; GO:0016325; F:apoptosis; IEA.
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR003109; BC12_BH4.
InterPro; IPR003109; BC12_Family.
InterPro; IPR003475; BC12_Family.
InterPro; IPR004725; BC12_reg.
Pfam; PF002452; BC1-2; 1.
Pfam; PF002180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H.; "A novel Bcl-x isoform connected to apoptosis in T cells."; Immunity 7:629-639(1997).
EMBL; U51278; AACG3459.1; --
EMSL; P53563; 1AF3.
                                                                                                                                                 TIGRFAMS; TIGR00865; bCl-2; 1.
PROSITE; PS50062; BCL2_PAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01258; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS50063; BH4 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O35844;
O35844;
O1-JAN-1998
O1-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=B6/CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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Bcl-xL.
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                                                                                  Similarity
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                                  RALVADFVGYKLRQKGY-----
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RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
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                                                                  Conservative
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Rodentia;
                                                                                                                                   26033 MW;
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                                                                                43.2%;
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                                                                Score 435.5;
Pred. No. 1.1e
22; Mismatches
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Last annotation updat
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Pred. No. 3.
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Sciurognathi; Muridae;
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                                                                                                                                    3083F2D8327E072E CRC64;
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                                                              1.1e-30;
ches 56;
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/ Murinae; Mus
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Best Local S
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Pfam; PF00180; BH4; 1.

SMART; SM00337; BCL; 1.

SMAXT; SM00265; BH4; 1.

PROSITE; PS01062; BC1-2; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01250; BH3; 1.

PROSITE; PS01260; BH4; 1.

SEQUENCE 233 AA; 26017 MW; (
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01-JUN-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Bcl-xl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR00393; Bcl2 BH4.
InterPro; IPR002475; Bcl2 family.
InterPro; IPR004725; Bcl2 reg.
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                                                                                                                                                                                                                                                                                         Similarity
97; Conserv
                                                                                                                                                                                                                                                        RALVADFVGYKLRQKGY----
                    NGGWDTFVELYGNNAAAESRK---
                                                                                                                 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
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                                                SGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                   QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                         43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              _FAMILY;
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                   -GQERSNRWFLTGMTVAG-VVLLGSLFSRK 233
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NGGWDTFVDLYGNNAAAESRKGKEGFNRWFLTGMTVAGVVLLGSL
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Last sequence update)
Last annotation update)
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Nagafuchi S., Sano J., Kano R., Hasegawa A.;
Nagafuchi S., Sano J., Kano R., Hasegawa A.;
"Moleculer cloning of feline Bcl-2 family.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AB080951; BAB65856.2; -.
EMBLG: 0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis; regulator activity
GO; GO:0006915; P:apoptosis; IEA. Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT RELVVDFLSYKLSOKGYSWSRFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV Score 433.5; Pred. No. 1.6e 23; Mismatches CD17F24FE9D47BC9 1.6e-30; DB 58; 9 databases ΙEΑ CRC64; Length Indels Euteleostomi; Felis. 233; 55 V----V Gaps 65 124 80 28 ທ ••

140

184

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RESULT 10
Q9MZS7
ID Q9MZS
AC Q9MZS
DT 01-OC
DT 01-OC
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DT 0
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Best Local S
Matches 94
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InterPro; IPR003093; Bc12_BH4.
InterPro; IPR003475; Bc12_Family
InterPro; IPR004725; Bc12_reg.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BC1; 1.
SMART; SM00337; BC1; 1.
SMART; SM00365; BH4; 1.
ITGRPAMS; TIGR00865; bc1-2; 1.
PROSITE; PS0062; BC1_2-FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH2; 1.
PROSITE; PS01259; BH2; 1.
PROSITE; PS01259; BH2; 1.
PROSITE; PS01259; BH4; 1.
                                                                                                 Q9MZS7;
Q9MZS7;
01-OCT-2000
01-OCT-2000
01-JUN-2003
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Q9N1A2;
Q1-OCT-2000
01-OCT-2000
01-JUN-2003
                                                                   Bcl-x long
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GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
      Eukaryota;
                                     Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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"PCR Cloning of a Por
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Lee T.L., Can
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   g protein.
(Sheep).
Metazoa;
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(TremBlrel. 15, Last sequence update)
(TremBlrel. 24, Last annotation updat
                                                                                                                                                                                                                                    PRELIMINARY;
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Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Bcl2_BH4.
; BCL2_family.
; Bcl2_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%;
                                                                                                 25,
24,
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                                                                                                 Last
Last
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Pred. No. 2.4e
21; Mismatches
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      Craniata;
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2FA312818B25E17D CRC64;
                                                                                                 sequence update)
annotation updat
                                                                                                                                                                                                                                    233
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      Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4e-30;
les 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
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                                                                                                 update)
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      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                                                                               229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 11
QBBQK4
ID 08B0K
AC 08B0K
AC 08B0K
DT 01-MA
DT 01-OC
B-Cel
GN B-Cel
GN Mus m
OC Eukax
OC Mamma
OX NCBI-
RN [1]
RP SEQUE
RC STRAI
RX MEDLI
RA The F
RA the P
RA the P
RT 60,77
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Best Local S
Matches 91
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PEAM; PF0045; BC1-2; 1.

PEAM; PF002180; BH4; 1.

SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

TIGRFAMS; TIGR00865; bC1-2; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01258; BH3; 1.

PROSITE; PS01250; BH4; 1; 1.

PROSITE; PS01260; BH4-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0016039; F:apoptosis regulator ac
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR000712; BC12_BH.
InterPro; IPR003093; BC12_BH4.
InterPro; IPR002475; BC12_family.
InterPro; IPR00475; BC12_family.
InterPro; IPR00475; BC12_reg.
                                                                                                                                                                                     Q8BQK4
Q8BQK4;
01-MAR-2003
01-MAR-2003
01-OCT-2003
the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
                                          STRAIN=C57BL/6J; TISSUE=Body; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               whirray J.F., Dong Y.B., Leig

"Bcl-x in the sheep ovary.",

Submitted (JUL-1999) to the

EMBL; AF164517; AAF89532.1;

HSSP; P53563; 1AF3.
                                                                                SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Caprinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                    142
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                                                                                                                                                                          leukemia/lymphoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                             VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                                                                                                                                                                                                                                                                                           GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                    GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                              VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN
                                                                                                                                                                                                                                                                                                                                                                                                                NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RALVADFVGYKLROKGY-----
                                                                                                                                                                       3 (TrEMBLrel. 23, 0
3 (TrEMBLrel. 23, 1
3 (TrEMBLrel. 25, )
kemia/lymphoma 2.
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                        ·------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                     Created)
Last seq
Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 428.5; DB 6;
Pred. No. 4.5e-30;
3; Mismatches 59;
                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         012BFA1382762915
                                                                                                                                                                                      sequence update) annotation updat
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                           Group
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                                                                                                                                                                                                                                           B
              OH,
                            Phase
                                                                                                                                                                                     update)
              hase I & II
functional
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              annotation
                            Team;
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                                                                                                                       Mus
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Q7TSNA
ID Q7TSN
AC Q7TSN
AC Q7TSN
AC Q7TSN
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
Rattu
OC Eukar
OC Mamma
OC NCBI
RN [1]
RN [1]
RN [1]
RP STRAI
RN Tanak
RA Tanak
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Best Local S
Matches 87
                                                               Query Match
Best Local S
Matches 87
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SMART; SM00265; BH4; 1.

TIGRAMS; TIGR00865; bCl-2; 1.

PROSITE; PS50062; BCL2; FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01259; BH4; 1.

PROSITE; PS01260; BH4; 1.

PROSITE; PS01260; BH4; 1.

PROSITE; PS01263; BH4; 2; 1.

PROSITE; PS01263; BH4; 2; 1.
                                                                                                                      STRAIN-Wistar;
Tanaka T., Nangaku M.;
Tanaka T., Nangaku M.;
"Rat Bc12-like protein.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF512835; AAP47159.1; -.
SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;
                                                                                                                                                                                                                                               Eukaryota; Mētazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                Q7TSN8;
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:88138; Bcl2.
GO; GO:0005829; C:cytcosol; IDA.
GO; GO:0008189; F:apoptosis inhibitor activity;
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005915; P:apoptosis; IDA.
                                                                                                                                                                                                                                                                                                Bcl2-like protein.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000712; Bcl2_BH.
InterPro; IPR003073; Bcl2_BH4.
InterPro; IPR003475; Bcl2_family.
InterPro; IPR004725; Bcl2_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 420:563-573 (2002)
EMBL; AK049473; BAC33767
MGD; MGI:88138; Bcl2.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               Q7TSN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142
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                                9
                                                               . Similarity
87; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALMMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPLRPLVATTGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
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DNREIVMKYIHYKLSORGYEWDAGDADAAPLGAAPTPGIFSFOPESNPMPAVHRDMAART
                              DTRALVADEVGYKLROKGYVCGAG-----PG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHRDMAART
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC33767.1; -.
                                                                            41.0%;
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37.5%;
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                                                                                                                                                                                                                                                                                                                                25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                           Score 413; DE
Pred. No. 1.1e
94; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 413; DB 11;
Pred. No. 1.1e-28;
                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B726BFFA3AA1C718 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                               236
                                                                            DB 11;
1.1e-28;
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                                                               59;
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                                                                                          Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 236;
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                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                               52;
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
 69
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                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wishiman K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villaion D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Kones S. T. Mayra W. A., Schmutz J., Myers R.M., Schein J.S.,

RA Kones S. T. Mayra W. A., Schmutz J., Schnerch A., Schein J.S.,

RA Kones S. T. Mayra W. A., Schmutz J., Schnerch A., Schein J.S.,

RA Kones S. T. Mayra W. A., Schmutz J., Schnerch A., Schein J.S.,

RA Kones S. T. Mayra W. A., Schmutz J., Schnerch A., Schein J.S.,

RA Kones S. T. Mayra W. A., Schmutz J., Schnerch A., Schein J.S.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
BC1-XL-like protein 1 (Bc121 protein).
GO; GO:0016329; F:apoptosis regulator GO; GO:0006915; P:apoptosis; IEA. InterPro; IPR000712; Bcl.2 BH. InterPro; IPR000393; Bcl.2 BH4. InterPro; IPR002475; BCl.2 family. Pfam; PF00452; Bcl.2 f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21299061; PubMed=11406282;

Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong Choning and characterization of zfBLP1, a Bcl-XL zebrafish, Danio rerio(1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii, Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprinidae; Dani
NCBI_TaxID=7955;
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                                                                                                                                      ZFIN;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Body;
                                                                                                                                                                                                                                                                                                              Proc.
                                                                                                                                                                                                                                                                                                                                                       Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=AB; TISSUE=Body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1519:127-133(2001).
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                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.
c. Natl. Acad. Sci. U.
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                                                                                                                            AF317837; AAK81706.1; -.
BC044130; AAH44130.1; -.
ZDB-GENE-010730-1; bc121
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                                                                                                                                                                                                   (JAN-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                      bc121.
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ta; Vertebrata; Euteleostomi;
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                                                                                                             activity;
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RESULT 15

Q9BDD5 PRELIMINARY; PRT; 180 AA.

AC Q9BDD5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 24, Last annotation update)
DT 01-JUN-2003 (TREMBLREL. 24, Last annotation update)
DE Anti-apoptotic regulator Bc1-xL (Fragment).
OS Bostaurus (Bovine).
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Best Local S
Matches 77
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Best Local Similarity 36.6
Matches 87; Conservative
                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
MEDLINE=22672518; PubMed=12787069;
Itch T., Itch A., Pleasure D.;
"Bcl-2-related protein family gene ey
differentiation.";
J. Neurochem. 85:1500-1512(2003).
EMBL; AY185099; AAO64469.1; -.
SEQUENCE 79 AA; 8602 MW; 47EDFB31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02180; BH4; 1.
SWART; SM00337; BCL; 1.
PROSITE; PS50062; BC12 FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS50063; BH4 2; 1.
SEQUENCE 238 AA; 26253 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003
01-0CT-2003
01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL-WS.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7TS61;
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                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                     TGAVALGALVTVGAFFASK 193
                                                                                                                                                                                     MEPLVGQVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVL
                                                                                                                                                                                                    MEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVL
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                                                                                                                                      TGAVALGALVTVGAFFASK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSGGWAEFTALYGDGALEEARRLREG--NWA-SVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FESVMDEVERDGVNWGRIVGLFAFGGALCVECVEKEMSPLVGRIAEWMTVYLDNHIQPWI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTQVSDELFQGGENWGRLVAFFVFGAALCAESVNKEWEFLVGQVQEWMVAYLETRLADWI
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                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                   39.9%;
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36.6%; Pred. No. 8
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                                                                                                                                                                                                                                      Score 402; DB Pred. No. 2.6e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation updat
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47EDFB3EE2909485 CRC64;
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.6e-28;
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                                                                                                                                                                                                                                                               Length
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Best Local S
Matches 76
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NON_TER
NON_TER
SEQUENCE
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"Characterization of the bovine bol-xL gene and related "Characterization of the bovine bol-xL gene and related submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF245488; AAX31307.1; -.
EMBL; AF245489; AAX31308.1; -.
EMBL; AF245489; AAX31308.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria
Bovidae; Bovinae;
NCBI_TaxID=9913;
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SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016329; F:apoptosis regulator GO; GO:0006915; P:apoptosis; IEA. InterPro; IPR002712; Bcl.2 BH. InterPro; IPR002475; BCL.2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
158
                                                        164
                                                                                                                                                98
                                                                                                                                                                                                                                         38
                                                                                                                                                                                                                                                                                                     44
                                                                                                                                                                                                                                                                                                                                                                    76;
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50062; BCL2 FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
                                                     E--GNWASVRTVLTGAVALGAL
                                                                                                                 GALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ 157
                                                                                                                                                                                                                                         QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG
                                                                                                                                                                                                                                                                                        QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG
ERFNRWFLTGMTVAGVVLLGSL
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180 AA;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20062 MW;
                                                                                                                                                                                                                                                                                                                                                                                             39.8%;
                                                                                                                                                                                                                                                                                                                                                                                          Score 401; DB 6
Pred. No. 9e-28;
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actyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95DC436F95DABDA6 CRC64;
179
                                                        183
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity;
                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEA
                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                163
                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                        103
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Search completed: March 25, 2004, 15:44:26 Job time : 37 secs

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Result
No.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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         07:
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-155-327G-7
1007
1 MATPASAPDTRALV
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      BCLW MOUSE
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BCLX CHICK
GELX HUMAN
BCLX HUMAN
BCLX HOUSE
BCLZ CHICK
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BCL2 CHICK
BCL2 HUMAN
BCL3 HUMAN
BAXA HUMAN
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0 homo sapien
0 mus musculu
9 african swi
5 african swi
                                                                                                                                                                                  1 homo sapien
4 homo sapien
3 mus musculu
0 rattus norv
2 homo sapien
6 caenorhabdi
3 bos taurus
3 bos taurus
4 homo sapien
5 coturnix co
9 homo sapien
7 caenorhabdi
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 xenopus lae
6 gallus gall
7 sus scrofal
7 sus scrofal
7 homo sapien
3 mus musculu
3 rattus norv
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8 bos taurus
0 rattus norv
7 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 homo sapien
8 cricetulus
8 xenopus lae
4 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
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	4 5	44	43	42	41	40	39	38	37	36	S.	υ 4
	79	79	79.5	79.5	80	82.5	82.5	83.5	85	85.5	87	98.5
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	541	396	872	872	541	3432	1440	660	275	358	3433	179
	μ	ы	μ	ш	H	μ	Н	H	Н	Н	ш	۳
ALIGNMENTS	FTCD_RAT	PORA PYRFU	SYA_STRR6	SYA STRPN	FTCD_MOUSE	POLG JAEVJ	POLG_JAEVN	SQHC BRAJA	DAPB_AGRT5	GLNA_LACSA	POLG KUNUM	EAR_ASFE4
			Q8dpc7 streptococc	Q97q48 streptococc	Q91xd4 m formimido			P54924 bradyrhizob	Q8uiv8 agrobacteri	P23712 lactuca sat	P14335 k genome po	Q07818 african swi

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cc	"Generation and initial analysis of more than 15,000 full-length	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;	J., Myers R.M.,	enko Y., Bouffard G.G.,	on E Ketteman M Madan & Rodricues S Sanches	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	quellano N.A., Peters G.J., Abramson R.D., Mullahy	Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz	Moore T., Max S.I., Wang J., Hsieh F., K., Farmer A.A., Rubin G.M., Hong L.,	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	E.A., Grouse L.H., Derge J.G.,	8257: DubMed=124779	SEQUENCE FROM N.A.	DNA Res. 3:321-329(1996).	" .	"Frediction of the coaing sequences of unidentified human genes, vi. The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced by		Nagase T., Seki N., Ishikawa KI., Ohira M., Kawarabayasi Y.,	TISSUE=Brain; MEDITNE=97191544: PubMed=9039502:	SEQUENCE FROM N.A.		a novel member of the bcl-2 family, pr	., Bernard O., Copelar	358615; PubMed=8761287;	SECULATION A MORA SINGER SINGE			LW OR KIAA0271.	sontosis regulator Bol-W (Bol-2-like 2	1997. (Rel. 35, Created) 1997 (Rel. 35, Last seguence	BCLW HUMAN STANDARD; PRT; 193 AA. Q92843;	J.T.T. 1 N. HUMAN

Skinner

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anti-apoptotic

brain,

colon,

cell lines and

restrictions

EMBL outstation

δn

collaboration

Copeland

N.G.,

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BCLW MOUSE

BCLW MOUSE

ID BCLW MOUSE

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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; $M00337; BCL; 1.

SMART; SM00265; BH4; 1.

PROSITE; PS50062; BCL2 FAMILY; 1.

PROSITE; PS50080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01260; BH4 1; 1.

PROSITE; PS01260; BH4 1; 1.

PROSITE; PS50063; BH4 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis.
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0008189; F:apoptosis inhibitor activity; GO; GO:000818; F:apoptosis; TAS. GO; GO:0007283; P:april-apoptosis; TAS. InterPro; IPR000712; Bc12_BH.

InterPro; IPR000712; Bc12_BH4.

InterPro; IPR003093; Bc12_BH4.

InterPro; IPR003093; Bc12_Family.

Pfam; PF00452; Bc12_; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D87461; BAA19666.1
EMBL; BC021198; AAH21198
HSSP; Q07817; IMAZ.
Genew; HGN:995; BCL2L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U59747; AAB09055.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 Bcl-2 homology 1 SIMILARITY: Contains 1 Bcl-2 homology 2 SIMILARITY: Contains 1 Bcl-2 homology 4 SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Expresse in a wide range of tissues, and salivary gland.
DOMAIN: BH4 domain seems to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601931;
                                                                                                                        181
                                                                                                                                                181
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                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                          193;
                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                     ы
                                                                                                                                                                                                                                                                                                      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                GALVTVGAFFASK 193
                                                                                                                                                                                                      OVOEWMVAYLETRIADWIHSSGGWAEFTALYGDGALEEARRIREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                                                         FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                        GALVIVGAFFASK 193
                                                                                                                                                                            QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                              FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                     MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                        9
85
136
193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFICITY: Expressed in almost all myeloid ide range of tissues, with highest levels in k
                                                                                                                                                                                                                                                                                                                                       100.0%; llarity 100.0%; Conservative 0;
(Rel. 35, Created)
(Rel. 35, Last seq
(Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                            AΑ;
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH21198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           29 B:
104 B:
151 B:
20774 MW;
 sequence up
                                                                                                                                                                                                                                                                                                                                                                                           BH4.
BH1.
BH2.
W; 3792243A50281761 (
                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                       Score 1007;
Pred. No. 1.1
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be involved
             update)
                                                      193
                                                      æ
                                                                                                                                                                                                                                                                                                                                                      .1e-83;
                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BH1)
(BH2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BH4)
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                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain.
) domain.
) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell lines
                                                                                                                                                                                                                                                                                                                                                                   193;
                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                     60
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                                                                                              Matches
                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                InterPro; IPR000712; Bc12_BH.
InterPro; IPR003093; Bc12_BH4.
InterPro; IPR002475; BCL2_family.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SWART; SM00337; BCL; 1.
                                                                                                                                                                                                             PROSITE; PS50062; BCL2_FAM:
PROSITE; PS01080; BH1; 1.
PROSITE; PS01280; BH2; 1.
PROSITE; PS01260; BH4 1; 1
PROSITE; PS50063; BH4_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/10J;
MEDLINE=98160183; PubMed=9500547;
ROSS A.J., Waymire K.G., Moss J.E., Parlow A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=96358615; PubMed=8761287;

Gibson L., Holmgreen S.P., Huang D.C., Berna
Jenkins N.A., Sutherland G.R., Baker E., Ada
"bcl-w, a novel member of the bcl-2 family,
Oncogene 13:665-675(1996).
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatic
the European Bioinformatics Institute. Thei
use by non-profit institutions as long a
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Russell L.D., Macgregor G.R.; "Testicular degeneration in Bolw-deficient mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis regulator Bcl-W (Bcl-2-like 2 protein) BCL2L2 OR BCLW.
                                                                                                                                                               DOMAIN
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                      Apoptosia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 Bcl-2 homology 1 SIMILARITY: Contains 1 Bcl-2 homology 9 SIMILARITY: Contains 1 Bcl-2 homology 4 SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Expressed in almost all myeloid
in a wide range of tissues, with highest levels in b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and salivary gland. DOMAIN: BH4 domain seems to be involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Genet. 18:251-256(1998). FUNCTION: Promotes cell survival
                                                                                                                                                                                                                                                                                                                                                                                                        U59746; AAB09056.1; -. AF030769; AAB86430.1; -.
               6
                                                                                                          Similarity
FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                        MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                        MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                            9
85
136
193
                                                                                           99.3%;
milarity 99.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Mouse)
                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Bc1212
                                                                                                                                                29 E
104 E
151 E
20790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                       FAMILY; 1.
                                                                                          ; Score 1000;
; Pred. No. 4.7
1; Mismatches
                                                                                                                                                BH4.
BH1.
BH2.
36CA185F5945DFB4 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernard O., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
                                                                                        1.7e-83;
                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BH1)
(BH2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promotes cell survival.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BH4)
                                                                                                                                                   CRC64;
                                                                                                                      Length
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domain.
domain.
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Indels

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Gaps

120 9 60 193;

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121

QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL

180 120

FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG

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                             Query Match
Best Local S
Matches 125
                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENLA
                                                                                                                       Apoptosis;
NON_TER
DOMAIN
                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, characterization and expression of two Xenopus bcl-2-like cell-survival genes.";
Gene 158:171-179(1995).
Gene FUNCTION: Could be the homolog of mammalian Bcl-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR1 XENLA
Q91827;
                                                                                                                                                                                                  SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                            Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis regulator Ri (XRI) (Fragment).
Xenopus laevis (African clawed frog).
Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                           DOMAIN
                                                                                                                                                             PROSITE; PS50062; BCL2_FAMILY;
                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cruz-Reyes J., Tata J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95331613; PubMed=7607538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )1-NOV-1997 (Rel. 35, Last
5-MAR-2004 (Rel. 43, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: Developmental regulation only occurs in the brain of mid-metamorphosic to post-metamorphosic tadpoles and adults, where an increase of several fold has been observed. SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain. SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain. SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION:
                               125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                             X82462; CAA57845.1; -. Q07817; 1MAZ.
    10
                                           Similarity
                                                                                                                                                                         PS01080; BH1; 1.
PS01258; BH2; 1.
TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                   IPR000712; Bcl2_BH.
IPR003093; Bcl2_BH4.
IPR002475; BCL2_family.
                                                                                120
171
207
228 /
                                                                                                                                                 Transmembrane.
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus.
                                                                                 ΑA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                      139
                                                                                186
227
25068
                                       64.2%;
                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bomolog of mammalian Bcl-W.
Membrane-bound (Potential).
                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                           Score 646.5; DB
Pred. No. 3.8e-51
l; Mismatches 3
                                                                             POTENTIAL.
C499D449A585F8A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                     DB 1;
                                                   Length
                                                     228;
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                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q078I6; Q08908;

01-FEB-1995 (Rel. 31, Created)

10-NOV-1997 (Rel. 35, Last sequence update)

15-MAR-2004 (Rel. 35, Last annotation update)

Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).

15-ELILI OR BCLLX OR BCL-X.

15-Gallus gallus (Chicken).

15-Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97264485; PubMed=9110311; Vilagrasa X., Mezquita C., Mezquita J. "Differential expression of bcl-2 and "spermatogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Hubbard White Mountain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boise L.H., Gonzalez-Garcia M., Postema C.E., I
Turka L.A., Mao X., Nunez G., Thompson C.B.;
"bol-x, a bol-2-related gene that functions as
of apoprotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM SHORT). MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                       apoptotic activity (By similarity).

SIMILARITY: Contains 1 Bcl-2 homology 1
SIMILARITY: Contains 1 Bcl-2 homology 3
SIMILARITY: Contains 1 Bcl-2 homology 3
SIMILARITY: Contains 1 Bcl-2 homology 4
SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                            Reprod. Dev. 47:26-29(1997).

FUNCTION: Dominant regulator of apoptotic cell death.

form displays cell death repressor activity, whereas
isoform promotes apoptosis (By similarity).

SUBCELLULAR LOCATION: Mitochondrial membranes and per
                                                                                                                                                                                                       development
DOMAIN: BH4
                                                                                                                                                                                                                               TISSUE SPECIFICITY: Highest expression in organs with lymphoid
                                                                                                                                                                                     function. Intact
                                                                                                                                                                                                                                                                      Name=Short
                                                                                                                                                                                                                                                                                                                                  envelope (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105
                                                                                                                                                                                                                                                    IsoId=Q07816-2;
                                                                                                                                                                                                                                                                                  IsoId=Q07816-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWNVAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRALVEDIVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LETNLRDWIQSNGGWNGFLTLYGDGAIBEARRQREGNWASLKTVLTGAVALGALMTVGAL
                                                                                                                                                                                                       BH4 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                     BH1 and
                                                                                                                                                                                                                                                    Sequence=VSP_000514;
                                                                                                                                                                                                    seems to be involved in the anti-apoptotic
                                                                                                                                                                                    BH2 domains are required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
                                                                                                                                                                                                                                                                                                                                                                                                                                                            bcl-x during chicken
                                                                                                           (BH1)
(BH2)
(BH3)
(BH4)
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domain.
domain.
                                                                                                                                                      domain
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L outstation -
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short
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its

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RESULT 5
BCLX PIG
ID COTT
AC 0777
AC 0777
DT 15-J
DT 15-J
DT 15-J
DT 15-W
DE Apor
GN BCL2
OS Sus
OC Euk
OC Mam
OC 
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMAXT; SM00337; BCL; 1.
SMAXT; SM00365; BH4; 1.
TIGRFAMS; TIGR00865; Bc1-2; 1.
PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01258; BH4 1; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS01260; BH4 1; 1.
                                                                                                                                                                                                                                              BCLX PIG
077737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000712; B
InterPro; IPR003093; B
InterPro; IPR002475; B
InterPro; IPR004725; B
SEQUENCE FROM N.A.

MEDINE=99171363; PubMed=10072723;

Bartling B., Hoffmann J., Holtz J.,

"Quantification of cardioprotective short-term hibernating myocardium.";
                                                                                                            15-UIL-1999 (Rel. 38, Created)
15-UIL-1999 (Rel. 38, Last sequence update)
15-UIL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
BCL2L1 OR BLC2L OR BCLX.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis;
DOMAIN
DOMAIN
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z23110; CAA80657.1; -. EMBL; U26645; AAB07677.1; -. PIR; A47537; A47537.
                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02180;
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                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                             186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P53563; 1AF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z23110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 41.7
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
                                                                                                                                                                                                                                                                                                                                                                         EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                                                                                                                                                                                                                                                                                                                                            LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RALVADEVGYKLROKGY-------------------------VCGAGPGEGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                        LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AADPHHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELVIDEVSYKLSORGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
125
176
185
                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH4;
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194
191
223
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41.7%;
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Bcl2_BH4.
BCL2_family.
Bcl2_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 432.5;
Pred. No. 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH1.
BH2.
POTENTIAL.
ERFYDLYGNNAAAELRKGQETENKWLLTGATVAGVLLLGSL
LSRK -> VRTALP (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP
                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTId=VSP_000514.
A97D3A4D04C0E9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                Schulz R., Heusch G., Darmer D.; gene expression in porcine
                                                                                                                                                                                                                                                              233
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1es 62;
                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                 Euteleostomi;
Sus.
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                                                                                                                                                                                                                                                                                                                                                                           193
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Best Local s
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TRANSMEM
SEQUENCE
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>:</del>
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ001203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                               82
                                                                                                                                σ
                                                                                                                                                                                               94;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                         129
129
180
210
233
                                                                                                                                                                                               Conservative
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envelope (By similarity).

-- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death.

-- PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has prospectic activity (By similarity).

-- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-- SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulate cell death by blocking the voltage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome o, from the mitochondrial membrane. SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) and apoptotic activity is inhibited by association with SIVA isofoli. Inhibits activation of caspases (By similarity). Appears to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31:147-158(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heterodimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L) anti-
isoform
                                 collaboration
outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                          death
                                                                                                                                                                                                                                                                                                                                                                      pro-
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TIGRFAMS; TIGRO0865; bcl-2; 1.

PROSITE; PS50062; BCL2_FAMILY; 1.

PROSITE; PS01080; BH; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01250; BH4_1; 1.

PROSITE; PS50063; BH4_1; 1. InterPro; IPR000712; B InterPro; IPR003093; B InterPro; IPR002475; B InterPro; IPR004725; B SMART; SM00337; BCL; SMART; SM00265; BH4; Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1 Q07817; 1MAZ. Mitochond CAA04597.1; -. 24 B. 100 B. 148 B. 195 B. 226 B. 26061 MW; BC12_BH. BC12_BH4. BCL2_family. BC12_reg. ion, POTENTIAL 18BF6FA0441912B2 CRC64;

125 11 RALVADFVGYKLROKGY---QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE CGAGPGEGPAAD-----PLHQAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRFT RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 21; Score 431.5; DB Pred. No. 9e-32; 1; Mismatches 57; Indels 53, Gaps V----140 80 9 124 28 4

41.8%; 42.9%;

DB 1;

Length

233;

Ç"

141

SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL

183

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RC TISSUS=LUMY,

RX MEDLINE=22388257; PubMed=12477932;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Polatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.",

RET Tugnal A.M., Marra M.A.,

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RESULT 6

BECLY HUMAN
ID MARMAN
ID THEMBOTO 11-FEBD
DT 01-FEBD
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                              MEDLINE=96170038; PubMed Cheng E.H.-Y., Levi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q07817; (92270),
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sedlak T.W.,
     INTERACTION WITH (
                                                                                                                                           Korsmeyer S
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95372373; PubMed=7644501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis regulator Bcl-BCL2L1 OR BCL2L OR BCLX.
Homo sapiens (Human).
                                                                                                               Bax-independent inhibition
                                                                                                                                                                                                                                                                                                                                          "Multiple Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM X(L)).
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MEDLINE=93364977; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inchara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74:597-608(1993).
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                                                                                     379:554-556 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A. (ISOFORM X (BETA)).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OCT-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             OF GLY-138, AND HETERODIMERIZATION
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                                                                                                                                                                                                                                                                                                                                    family
     SIVA.
; PubMed=12011449
                                                                                                                                                                                                                                                                              Sci.
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vine B., Boise L
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MEDLINE=9818550; PubMed=9435230;
Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.
Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., V
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Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E
Eberstadt M., Yoon'H.S., Shuker S.B., Chang B.S., Minn A.J.,
Thompson C.B., Fesik S.W.;
"Structure of Bcl-xL-Bak peptide complex: recognition between
regulators of apoptosis.";
Science 275:983-986(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE
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- SIMILARITY: Belongs to t
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DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage dependent amion channel (UDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-X(S) isoform promotes apoptosis.

SUBUNIT: Bcl-X(L) forms beterodimers with BAX, BAK and Bcl-2. Heterodimerization with BAX does not seem to be required for antiapoptotic activity. Isoform Bcl-X(L) binds to Siva isoform 1.

SUBCLIJULAR LOCATION: Mitochondrial membranes and perinuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named iso Name=Bcl-X(L); IsoId=Q07817-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dulation of cell death bx Bcl-xL through cac. Natl. Acad. Sci. U.S.A. 95:554-559(1998) FUNCTION: Potent inhibitor of cell death.
                                             European Bioinformatics Institute.
                                                                                                                                                                                                      activity
                                                                                                                                                                                                                                                                                                                                                                                             Name=Bcl-X(beta);
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IsoId=Q07817-2;
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                                           SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
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InterPro; IPR003093; Bc12 BH4.
InterPro; IPR004775; BC12 family.
InterPro; IPR004775; BC12 reg.
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Pfam; PP00452; Bc1-2; 1.
SMART; SM00337; BC1; 1.
SMART; SM00337; BC1; 1.
SMART; SM00337; BC1; 1.
PR0SITE; PS010865; bC1-2; 1.
PROSITE; PS01259; BH3; 1.
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PIR; JE0203; JE0203;
PDB; LEXL; 29-CCT-97.
PDB; LEXL; 21-APR-97.
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13-JUN-01.
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P:anti-appicosis; TAS.
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D->A: NC
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VGDVDS (in isoform Bcl-X(beta)).
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HETERODIMERIZATION WITH BAX.
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A Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N., A Ohta S., Seldin M.F., Nunez G.;
"Genomic organization, promoter region analysis, and chromosome incendence organization of the mouse bel-x gene.";
L. Immunol. 158:4750-4757(1997).
C. -!-FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-promoter activity is inhibited by association with SIVA isoform in Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.
C. -!- SUBUNIT: Bcl-X(S) isoform promotes apoptosis.
C. -!- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimers heterodimers with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).
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MEDLINE=98051053; PubMed=9390687;

Yang X.-F., Weber G.F., Cantor H.

"A novel Bcl-x isoform connected of

apoptosis in T cells.";

Immunity 7:629-639(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95052604; PubMed=7963517; Fang W., Rivard J.J., Mueller D.L.,
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Mammalia; Eutheria; Rodentia;
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Eukaryota; Metazoa;
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MEDLINE=97289584; PubMed=9144489;
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Development 120:3033-3042(1994).
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                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michaud
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Sciurognathi; Muridae; Murinae;
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SMART; SM0033; BCL; 1.
SMART; SM00255; BH4; 1.
TIGREAMS; TIGRO0865; bcl-2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH2; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                     EMBL; X83574; CAA58557.1; -.
EMBL; L35049; AAA51039.1; -.
EMBL; L35049; AAA51040.1; -.
EMBL; U10102; AAA82174.1; -.
EMBL; U10101; AAA82173.1; -.
EMBL; U10100; AAA82172.1; -.
EMBL; U51279; AAC55460.1; -.
EMBL; U78031; AAB96881.1; JOIN
PIR; 149055; 149055.
                         Apoptosis;
DOMAIN
DOMAIN
                                                                      PROSITE;
  DOMAIN
DOMAIN
                                                                                                                                                                                              Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                   InterPro; IPR000712; Bcl2 BH.
InterPro; IPR003093; Bcl2 BH4.
InterPro; IPR002475; Bcl2 family.
InterPro; IPR004725; Bcl2 reg.
                                                                                                                                                                                                                                                                                  MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
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                                                                                                                                                                                                                                                                                           ; 149055; 149055.
; 149056; 149056.
; 149057; 149057.
; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptotic activity (By similarity).

SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1)
SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2)
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3)
SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4)
SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: The BH4 domain is required for anti-apoptotic acti
The BH1 and BH2 domains are required for both heterodimeri
with other Bc12 family members and for repression of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    postnatal
DOMAIN: Th
                                                                                                                                                                                                                                                                                 MGI:88139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Proteolytically cleaved by caspases during similarity). The cleaved protein, lacking the BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: Bcl-X(beta) is expressed in and postnatal tissues, whereas Bcl-X(L) is predom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=064373-4; Sequence=VSP 000519; TISSUE SPECIFICITY: Widely expressed, with highest levels in the brain, thymus, bone marrow, and kidney. Bcl-X(L) and Bcl-X(delta-TM) expression is enhanced in B and T lymphocytes that have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=BCL-X(delta-TM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=BCL-X(beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BCL-X(S);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope for Bcl-X(L). Cytoplasmic for Bcl-X(delta-TM). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                           PF00452; Bcl-2;
PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q64373-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q64373-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q64373-1; Sequence=Displayed;
                                                   PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
; Mitochondrion; Al
  4
86
129
180
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                                                                                                                                                                                                                                                                                 Bc121.
 100
148
195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=VSP_000517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence=VSP_000518;
                                                        Alternative
                                                                                                                                                                                                                                                                                                                                                   JOINED.
BH4
BH3
BH1
BH2
                                                      splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib
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predominantly
                                                        Transmembrane.
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domain.
domain.
domain.
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heterodimerization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis
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Best Local &
Matches 93
STRAIN-Sprague-Dawley; TISSUE-Ovary; MEDLINE-95129487; PubMed=7828536; Tilly J.L., Tilly N.I., Kenton M.L., Johnson A.L.; "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulos cell apoptosis is associated with decreased bax and constitutive
                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
Wesselingh S.L., David G
Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECLX RAT STANDARD; PRT; 23 AA. P53563; P70613; P70614; Q62678; Q62836; Q64087; Q01-OCT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Apoptosis regulator Bcl-X (Bcl-2-like 1 protein). BCL2L1 OR BCLX.
                                                                                                                                                                                                unspliced RNA,
                                                                                                                                                                                                                        "An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
Michaelidis T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAT
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                                                                                                                                                                                                                                       Shiraiwa N., Inohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                               MEDLINE=96278736; PubMed=8662675;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                       FISSUE=Thymus;
                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A. (ISOFORMS X(L)
                                                                                                                                                                             Biol.
                                                                                                                                                                                                                      raiwa N., Inohara N., Okada S. additional form of rat Bcl-x,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
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                                                                                                                                      FROM N.A. (ISOFORMS X(L)
                                                                                                                                                                               Chem.
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126
                                                                                                                                                                      rorm of rat Bcl-x, Bcl-xbeta, ger promotes apoptosis in promyeloid 271:13258-13265(1996).
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41.3%;
                                                                                                                                                                                                                                                                                                                                             G.L., Choi S., Veliuona
o the EMBL/GenBank/DDBJ o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL,
Missing (in isoform BCL-X(S)).
/FTId=VSP_000517.
DTFYULYGNNAAAESRKGQERENRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 428.5;
Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCL-X(delta-TM)).
/FTId=VSP_000519.
24D2AC79887E072E
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                       Yuzaki M.,
                                                                                                                                      X(S)).
                                                                                                                                                                                                                                                                                                      X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    x(s)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .7e-31;
ies 57;
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                                                                                                                                                                                                                  , Shoji S.-
generated
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databases.
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                                                                                                                                                                                                shoji S.-I.,
enerated by a
l cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                     Hardwick J.M.;
          ition of granulosa constitutive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233;
                                                                                                                                                                                                                      an
                                                                                                                                                                                                                                       Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53,
                                                                                                                                                                                                                                         S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
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PIR; S51761; S51761.

PDB; 1A83; O7-JUL-97.

InterPro; IPR000712; Bc12_BH.

InterPro; IPR003093; Bc12_BH4.

InterPro; IPR002475; BC12_family.

InterPro; IPR004725; Bc12_reg.

Pfam; PF00452; Bc1-2; 1.
                                                                                                                                                   EMBL; X82537; CAA57886.1; --
EMBL; X82537; CAA57887.1; --
EMBL; U10579; AAA19257.1; --
EMBL; U72350; AAB17353.1; --
EMBL; U72349; AAB17352.1; --
EMBL; U34963; AAA77686.1; --
EMBL; U34963; AAA77686.1; --
EMBL; S78284; AAC60702.1; --
PIR; 157431; 167431.
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstations the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98010630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure the Bcl-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aritomi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channnel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-X(S) and Bcl-X(beta) isoforms promote apoptosis.

SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).

SUBCELIULAR LOCATION: Mitochondrial membranes and perinuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P53563-3; Sequence=VSP 000521;
TISSUE SPECIFICITY: Expressed in most tissues. Bcl-X(beta) is specifically expressed in cerebellum, heart, and thymus. In the ovary, the predominant form is Bcl-X(L), with a small but detectable level of Bcl-X(S).

DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) antiapoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Bc1-X(beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Bcl-X(S);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Bcl-X(L);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       envelope (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P53563-2; Sequence=VSP_000520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P53563-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structure of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunishima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).

(By similarity).

(BH1)

(Contains 1 Bc1-2 homology 2 (BH2))

(Contains 1 Bc1-2 homology 2 (BH2))

(Contains 1 Bc1-2 homology 3 (BH3))

(Contains 1 Bc1-2 homology 4 (BH4))

(Contains 1 Bc1-2 family.
                Bcl-2;
BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272:27886-27892 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9346936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splicing; Named isoforms=3;
                                                                                                                                                                                   ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-xL. Implications for the function
                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain.
domain.
domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration -
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RESULT 9
BCL2_CHICK
ID BCL2_CHICK

STANDARD

PRT;

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                                                                                                           Matches
                                                                                                                 Query Match
Best Local :
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TIGRPAMS; TIGR00865; BROSITE; PS50062; B
PROSITE; PS01080; B
PROSITE; PS01258; B
PROSITE; PS01259; B
PROSITE; PS01260; B
PROSITE; PS01260; B
PROSITE; PS01260; B
                                                                                                                                    TURN
HELIX
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DOMAIN
TRANSMEM
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TURN
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                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis; Mi
3D-structure.
                          125
185
              141
                                       81
                                                     66
                                                                                             11
                                                                   29
                                                                                σ
                                                                                                                 Similarity
                                                                CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                             RALVADFVGYKLRQKGY-----V
NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
            SGGWAEFTALYGDGALEBARRLRE--GNWASVRTVLTGAVALGAL
                          QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEFWIQE
                                      QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                    NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                              RELVVDFLSYKLSOKGYSWSOFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                   185
187
233
                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       265; BH4; 1.
IGR00865; bc
                                                                                                           Conservative
                                                                                                                                                                 129
129
129
120
                                                                                                                                    ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                BCL2_FAMII
BH1; 1.
BH2; 1.
BH3; 1.
BH4_1; 1.
BH4_2; 1.
                                                                                                                                           24
100
148
195
226
                                                                                                                 42.6%;
                                                                                                                                    26158 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 _FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing; Transmembrane;
                                                                                                         22;
                                                                                                         Score 428.5; DB 1;
Pred. No. 1.7e-31;
2; Mismatches 57;
                                                                                                                                                                                                                                                                   BH4.
BH3.
BH1.
BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                   Missing (i
                                                                                                                                                                                                                                                                  /FTId=VSP 000521.

F -> Q (IN REF 1).
F -> S (IN REF 2).
A -> E (IN REF 2).
I -> L (IN REF 4).
FF -> SS (IN REF 4).
A -> T (IN REF 4).
A -> P (IN REF 4).
                                                                                                                                                                                                                                                                                                                        IDYSGDIPGLL (in isoform /FTId=vsp_000521.
                                                                                                                                                                                                                                                                                                                                     DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                    2B62B6C63864BC8F CRC64;
                                                                                                                                                                                                                                                                                                                                                           äŢ
                                                                                                                                                                                                                                                                                                                                                          isoform
                                                                                                                                                                                                                                                                                                                                                          Bc1-x(s).
                                                                                                          Indels
                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                Bcl-X(beta))
              183
                                                                                                                        233;
                                                                                                          53,
                                                                                                         Gaps
                           184
                                       140
                                                                  80
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or send a
Pfam;
SMART;
                                                                                                                                                 PIR;
                                                                                                                                                                                    EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                     This SWI
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01-APR-1993
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                        the
                                          InterPro; IPR000712; Bc12 BH.
InterPro; IPR003093; Bc12 BH4.
InterPro; IPR002475; Bc12 family.
InterPro; IPR004725; Bc12 reg.
                                                                                                                                                                                                                                                                                                 modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_
                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cazals Hatem D.L., Louie D.C., Tanaka S., Ree "Molecular cloning and DNA sequence analysis homologue of the Bel-2 oncoprotein."; Biochim. Biophys. Acta 1132:109-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=B-cell lymphoma;
MEDLINE=92379084; PubMed=1511008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92375724;
Eguchi Y., Ewert I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and
                                                                                                                          3L; D11382; BAA01978.1; J

3L; D11381; BAA01978.1; J

711961; CAA78018.1; J

311961; S24390; S24490; S24490; S24490; S24490; S24490; S24490; S24490; S24490; S244900; S24490; S24490; S24490; S24490; S24490; S24490; S24490; S244
                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nn Y., Ewert D.L., Tsujimoto Y.;
Nation and characterization of the chicken
variety of tissues including lymphoid and
t and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TaxID=9031;
                                    PF00452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sis regulator . RCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gallus (Chicken).
                                                                                                                                                                                                                                                       non-profit institutions as low d and this statement is not removes requires a license agreement (s an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
             BH4; 1.
                                  Bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1508712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bc1-2.
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Last seq
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                                                                                                                                                                                                                                                                          (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bcl-2 gene: expression neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                 collaboration
                                                                                                                                                                                                                                                                          .ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMUULLINGS, LICENTIGREAMS; TIGRO0865; BCL2 PAROSITE; PS01080; BH1; 1 PROSITE; PS01258; BH2; 1 DR PROSITE; PS01259; BH3; 1 DR PROSITE; PS01260; BH4] PROSITE; PS01260; BH4]
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2_BOVIN STANDARD
BCL2_BOVIN STANDARD
002718;
16-0CT-2001 (Rel. 40, C
16-0CT-2001 (Rel. 40, L
15-MAR-2004 (Rel. 43, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis BCL2.
                       -
                                                                                                                                                                                      "Increased ratio of bcl-2/bax expression is associated with leukemia virus-induced leukemogenesis in cattle."; Virology 242:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis;
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                       -
                                                                                                                                                                                                                                                  Reyes R.A., Cockerell
                                                                                                                                                                                                                                                                   MEDLINE=98162580; PubMed=9501056;
                                                                                                                                                                                                                                                                                         STRAIN=Holstein;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                     1)
JEQUENCE FROM N.A.
TISSUE=Thymus;
THEATH TO THE THEATH 
the apoptosis-activating factor (APAF-1) (By similarity) SUBUNIT: Forms homodimers, and heterodimers with BAX, BAI Bcl-X(L). Heterodimerization with BAX requires intact BHI
                                                       FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding release of cytochrome c from the mitochondria and/or by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
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                                                                                                                                                                                                                                                                                                                                                                              Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEFTALYGDGALEEARRIREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNREIVLKYIHYKLSORGYDWAAGEDRPPVPPAPAPAAAAPAAVAAAGASSHHRPEPPGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTRALVADEVGYKLROKGYVCGAG----PGEGPAADP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00265; BH4; 1.
TIGR00865; bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
139
233 AA;
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BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH2; 1.
BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                              Bos.
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13, Last
Bcl-2.
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139
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149
196
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64
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_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 423.5; DB Pred. No. 4.7e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ១ ដ
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E -> S (IN REF. 2
GSAAASEVPPAEGLRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> T (IN REF. 2)
-> V (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                Bovoidea;
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                                                                                                                                                                                                                               bovine
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K and
BH2
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Matches 86
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                                                                                                                                                                                                                                                                                                                                                                                                                     SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH4_1; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
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SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interacts with 1 - SUBCELLULAR LOCA membrane of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: Proteolytically cleaved by caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
DOMAIN: The BH4 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RAF-1 and TP53BP2 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellul membrane of the nuclear envelope and the endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinases. Dephosphorylated by protein phosphatase 2A (PP2A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q07817; 1MAZ
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SM00265; BH4;
                                                                                                                                                                                                      φ
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                          DTRALVADFVGYKLRQKGYVCGAG-----
AAAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFR
                                                                                                                                  DNREIVMKYIHYKLSQRGYEWDAGDAGAAPPGAAPAPGILSSQPGRTPAPSRTSPPPPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR00865; bcl-2;
                                                             GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQ
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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BC12_BH4.
BCL2_family.
BC12_reg.
                                                                                                                                                                                                                                                                                                               41.48;
38.28;
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                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ALA.
BH3.
BH1.
BH2.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POSPHORYLATION (BY PKC) (BY SPHOSPHORYLATION (BY PKC) (BY PK
                                                                                                                                                                                                                                                                                                            Score 416.5; DB Pred. No. 2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                           59;
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                                                                                                                                                                                                                                                                                                                                         Length
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(BY SIMILARIT
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c reticulum (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
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RESULT 11
BCL2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Expression of members of the bcl-2 gene family in the immature : ovary: equine chorionic gonadotropin-mediated inhibition of granucell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels."; [3]
membrane of the nuclear envelope and the endoplasmic reticulum.

-! TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.

-!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

-!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P49950; Q62837; Q64032;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Castren E., Ohga Y., Berzaghi M.P., Lindholm D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94193015; PubMed=8144041;
Sato T., Irie S., Krajewski S., Reed J.C.;
"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95059917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adult rat brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "bcl-2 messenger RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 19-172 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSUE=Brain
                                                                                                                                                                                                                                    the apoptosis-activating factor (APAF-1).
SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RAF-1 and TP53BP2 (By similarity).
SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrian membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=7969891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is localized in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
     pr-stimulated phosphorylation
anti-apoptosis activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
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                                                                                                              in the neuroepithelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the immature rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thoenen H.,
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Best Local S
Matches 84
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PROSITE; PS01080; BH1; 1
PROSITE; PS01258; BH2; 1
PROSITE; PS01259; BH3; 1
PROSITE; PS01260; BH4 1;
PROSITE; PS50063; BH4 2;
                                                                                                                                                                                                                                                                                                                                                MOD RES
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

-!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH2) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
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DOMAIN
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EMBL; U34964; AAA77687.1; -.
EMBL; U34964; NOT ANNOTATE
EMBL; S74122; -; NOT ANNOTATE
PIR; 153744; 153744.
PIR; 167432; 167432.
USCR. 06732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000712; Bcl2 BH.
InterPro; IPR003093; Bcl2 BH4.
InterPro; IPR002475; BCL2 family.
InterPro; IPR004725; BCL2 reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entitles requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00337; BCL; 1.
SM00265; BH4; 1.
Ms; TIGR00865; bcl-2;
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                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                  Similarity
VVEELFROGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and this statement is not removed. Usage by and the statement is not removed. Usage by and the statement (See http://www.isb-sib.ch/announce/
                                        VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                                                                    SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                     DNREIVMKYIHYKĹSORGYEWDTGDEDSAPLRAAPTPGIFSFOPESNRTPAVHRDTAART
                                                                                                                                                                                                                   DTRALVADEVGYKLROKGY-----
                                                                                                                                                                                                                                                                                                                                                     236 AA;
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                                                                                                                                                                                                                                                              Conservative
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                                                                                                                        -VCGAGPGEGPAADPLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFTQ
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BH4_2; 1.
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36.2%;
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                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion; Phosphorylation
                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                BH4.
BH3.
BH1.
BH2.
POTENVIAL.
POTENVIAL.
POTENVIATION (BY PKC)
PHOSPHORYLATION (BY PKC)
A -> R (IN REF. 2).
S -> Y (IN REF. 2).
S -> Q (IN REF. 2).
                                                                                                                                                                                                                                                           Score 414; DB 1;
Pred. No. 3.4e-30;
4; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                  -> Q (IN REF. 2)
E7688CB9071A872A
                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                  CRC64;
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L outstation -
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RESULT 12
BCL2_MOUSE
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01-MAR-1989 (Rel. 10, C
01-APR-1993 (Rel. 25, I
15-MAR-2004 (Rel. 43, I
                                                                                                                                                                -
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069407; PubMed=9852076;
Deng X., Ito T., Carr B., Mumby M.,
"Reversible phosphorylation of Bel2
bryostatin 1 is mediated by direct i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES. MEDILINE=97277291; PubMeda9115213; Ito T., Deng X., Carr B., May W.S. Jr.; "Bcl-2 phosphorylation required for anti-apoptosis function."; J. Biol. Chem. 272:11671-11673(1997).
                                                                                                                                                                                                                                                                                                                                                                                                        phosphatase 2A*.";
J. Biol. Chem. 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92375724; PubMed=1508712; Eguchi Y., Ewert D.L., Tsujimoto Y. "Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in a variety of tissues including lymphoid adult and embryo."; nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbcl-2: structure and expression of the gene homologous to the human gene involved in follicular lympho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis regulator Bcl-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCL2 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 221-222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                IsoId=P10417-2; Sequence=VSP 000513; TISSUB SPECIFICITY: Expressed In a var DOMAIN: The BH4 domain is required for interaction with RAF-1.
                                                                                                                                          membrane of the nuclear ALTERNATIVE PRODUCTS: Event=Alternative splici
                                                                                                                                                                                                                      caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding the apoptosis-activating factor (APAF-1).

SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK ar Bcl-X(L). Heterodimerization with BAX requires intact BHI and BHZ domains, and is necessary for anti-apoptotic activity. Interacts with TP53BP2 (By similarity). Also interacts with APAF-1 and
                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 273:34157-34163(1998).
FUNCTION: Suppresses apoptosis in a variety of cell systems FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with
                                                                                                                                                                             SUBCELLULAR LOCATION: membrane of the nuclea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49:455-463 (1987).
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                                                                                                              IsoId=P10417-1;
   Phosphorylation/dephosphorylation apoptotic activity. Growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY PP2A.
PubMed=9852076;
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Last sequence update)
Last annotation updat
                                                                                                                                             splicing; Named isoforms=2;
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following interleukin
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phoid and
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                                               variety of tissues. for anti-apoptotic
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neuronal organs in
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                regulates
regulates Bcl2 phosphorylation
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Best Local S
Matches 87
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GO; GO:0005829; C:cytosol; IDA.

GO; GO:0008189; F:apoptosis inhibitor activity; IDA.

GO; GO:0008189; F:apoptosis inhibitor activity; IDA.

GO; GO:0008189; F:apoptosis; IDA.

InterPro; IPR000712; Bcl2 BH.

InterPro; IPR000712; Bcl2 BH4.

InterPro; IPR0002475; Bcl2 BH4.

InterPro; IPR0004725; Bcl2 FBH4.

InterPro; IPR004725; Bcl2 FBH4.

Pfam; PF00482; Bcl-2; 1.

Pfam; PF00452; Bcl-2; 1.

Pfam; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO0865; bcl-2; 1.

PROSITE; PS50062; BCL2 FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01289; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01250; BH4 1; 1.

PROSITE; PS01260; BH4 1; 1.

PROSITE; PS01260; BH4 1; 1.
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VARSPLIC
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                           TRANSMEN
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Phosphorylation
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HSSP; Q07817; 1MAZ.
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EMBL; M16506; AAA37282.1;
EMBL; M16506; AAA37281.1;
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                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoting further caspase activity.

SIMILARITY: Contains 1 Bcl-2 homology 1
SIMILARITY: Contains 1 Bcl-2 homology 3
SIMILARITY: Contains 1 Bcl-2 homology 3
SIMILARITY: Contains 1 Bcl-2 homology 4
SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bc12 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A).

PTM: Proteclytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol
                                                        10
 70
                             35
                                                                                                               l Similarity
87; Conser
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                                                                              DTRALVADFVGYKLRQKGYVCGAG------PG----
SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSOLHLTPFTARGRFAT
                                                     DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART
                                                                                                                                                                        236
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90
133
184
209
34
70
                                                                                                               Conservative
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                       EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
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104
152
199
230
230
70
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BH3.

BH1.

BH2.

POTENTIAL.

CLEAVAGE (BY CASPASES) (BY SIMILARITY).

PHOSPHORYLATION (BY PKC).

DAFVELYGESMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                                               34;
                                                                                                                             Score 413;
Pred. No. 4
                                                                                                                                                                                                   GHK -> VGACLVE (in isoform
                                                                                                                                                                                       /FTId=VSP
                                                                                                                                                                      TId=VSP_000513,
AA85EF6B0766BE0A_CRC64;
                                                                                                               Mismatches
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(BH2)
(BH3)
(BH4)
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                                                                                                                                                                                                                                                                                                                                                 Mitochondrion;
                                                                                                                                          Length 236;
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RESULT
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Tsujimoto Y., Croce C.M.;
"Analysis of the structure, trar
"Analysis of the involved in humbel-2, the gene 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM ALPHA).

MEDLINE-88196071; PubMed=2834197;
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Klausmer R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-87002488; PubMed-2875799;
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"Cloning and structural analysis of cDNAs for k
2/immunoglobulin transcript resulting from the
translocation.";
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P10415; P10416; Q13842; Q16197;
01-MAR-1989 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43. Rieder M.J., Livingston R.J., Daniels M.R., Chur Rieder M.Z., Livingston R.J., Daniels M.R., Poel C.L., Robertson Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translocation.";
Cell 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a
                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
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TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2003) to
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MEDLINE=87002488; I
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
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protein kinase pathway normally activated at G(2)/M.";

Mol. Cell. Biol. 19:8469-8478(1999)
-1- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoletic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Naumovski L., Cleary M.L.;
"The p53-binding protein 53BP2 also interacts
"The pc3-binding protein 53BP2 also interacts
cell cycle progression at G2/M.";
Mol. Ceil. Biol. 16:3884-3892(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION by ADMINISTRATION BY PUMMed=10567572;
WEDLING=20036804; PubMed=10567572;
Yamamoto K., Ichijo H., Korsmeyer S.J.;
"BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal "BCL-2 is phosphorylated and inactivated at G(2)/M.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21260650; PubMed=11368354; Ruvolo P.P., Deng X., May W.S.; "Phosphorylation of Bcl2 and regulation the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE=94239528; PubMed=8183370;
Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
"BHI and BHZ domains of Bcl-2 are requinapoptosis and heterodimerization with Bunature 369:321-323(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON-HODGKIN'S LYMPHOWA SER-59 AND ILE-93. MBDLINE=92096610; PubMed=1339299; Tanaka S. Louie D.C., Kant J.A., Reed J.C.; "Frequent incidence of somatic mutations in oncogenes of non-Hodgkin's lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96251339; PubMed=8668206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98057466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 348:334-336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hockenbery D., Nunez G., Milliman "Bcl-2 is an inner mitochondrial programmed cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91066924;
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the apoptosis-activating factor (APAF-1).
SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD,
Bcl-X(L). Heterodimerization with BAX requires intact BH1 a
domains, and is necessary for anti-apoptotic activity (By
similarity). Also interacts with APAF-1, RAF-1 and TP53BP2.
SUBCELLULAR LOCATION: Outer mitochondrial membrane, intrace
membrane of the nuclear envelope and the endoplasmic reticu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E.H.-Y., Kirsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sion of Bcl-2 to a Bax-like death effector by caspases.", 278:1966-1988(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WITH TP53BP2
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rsch D.G., Clem R.J., Ravi R.,
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nez G., Milliman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISOFORM ALPHA),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis.";
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and BH2
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Matches 87
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EMBL; M13995; AAA51814.1; ALT_SEQ.
EMBL; M14745; AAA35591.1; -.
EMBL; X06487; CAA29778.1; -.
EMBL; AY220759; AA026045.1; -.
EMBL; BC027258; AAH27258.1; -.
EMBL; BC027258; AAH27258.1; -.
EMBL; S72602; AAD14111.1; ALT_SEQ.
PIR; B29409; TVHUB1.
PIR; C37332; TVHUB1.
                                                                                                                          InterPro; IPR000712; Bc12 BH.
InterPro; IPR003093; Bc12 BH4.
InterPro; IPR002475; BC12 family.
InterPro; IPR004725; Bc12 reg.
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PDB; 1GJH; 13-JUN-01.
Genew; HGNC:990; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                               GO:0005743; C:mitochondrial inner membrane; GO:0008189; F:apoptosis inhibitor activity; GO:0006916; P:anti-apoptosis response; TAS. GO:0006959; P:humoral immune response; TAS. GO:0008285; P:negative regulation of cell pr GO:0000074; P:regulation of cell cycle; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transitions.

SIMILARITY: Contains 1 Bcl-2 homology 2 (BH1)
SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2)
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3)
SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4)
SIMILARITY: Belongs to the Bcl-2 family.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

DISEASE: Involved in follicular lymphoma (FL) (also known as type thronic lymphatic leukenta) by a chromosomal translocation t(14;18) (q32;q21) which involves BCL2 and immunoglobulin gene regions. BCL2 mutations found in non-Hodgin's lymphomas carrying the chromosomal translocation could be attributed to the Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity) Proteolytically cleaved by caspases during apoptosis. The
                                                                                                                                                                                                                                                                                                               151430; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WWW="http://www.infobiogen.fr/services/chromcancer/Genes/BCL2ID49.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              somatic hypermutation mechanism resulting in nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: The BH4 domain is for interaction with RAF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
Event=Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Phosphorylation/dephosphorylation on Ser-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P10415-2; Sequence=VSP 000512; ISSUE SPECIFICITY: Expressed in a vari
MAIN: The BH4 domain is required for
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                                                         87;
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                                                                          Similarity
DTRALVADFVGYKLRQKGYVCGAG----
                                                         Conservative
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                                                                        41.0%;
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                                                         34;
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Pred. No. 4.
                                                       Mismatches
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4.7e-30;
nes 59;
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Q9JJV8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seguence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                            the appoptosis-activating factor (APAP-1) (By similarity).

-!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAA, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-appototic activity. Also interacts with APAP-1, RAF-1 and TP53BP2 (By similarity).

-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

-!- DOMAIN: The BH4 domain is required for anti-appototic activity and for interaction with RAP-1 (By similarity).

-!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-appoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-appotosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A) of the similarity in the cell cycle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., MEDLINE=21092839; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.";
Biochem. Biophys. Res. Commun. 275:899-903(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20431763; PubMed=10973819; Tomicic M.T., Christmann M., Kaina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cricetulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10030;
PIN: Protectly ically cleaved by caspases du cleaved protein, lacking the BH4 domain, ha activity, causes the release of cytochrome promoting further caspase activity.

SIMILARITY: Contains 1 Bc1-2 homology 1 (BH SIMILARITY: Contains 1 Bc1-2 homology 2 (BH SIMILARITY: CONTAINS 1 BC1-2 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chem. Biophys. Res. Commun. 281:404-408(2001).
FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding trelease of cytochrome c from the mitochondria and/or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caspase-3.";
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaina
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XENLA AR11 XEI Q91828;

XENLA

STANDARD;

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Xenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopus

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-NAR-2004 (Rel. 43, Last annotation
Apoptosis regulator R11 (XR11)

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Best Local
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InterPro; IPR002475; Bd
InterPro; IPR004725; Bd
InterPro; IPR004725; Bd-2; I
Pfam; PF00452; Bd-1-2; I
Pfam; PF02180; BH4; 1.
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-!- SIMILARITY: !
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50062; BCL2
PROSITE; PS01080; BH1;
PROSITE; PS01258; BH2;
PROSITE; PS01259; BH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00265; BH4; TIGRFAMS; TIGRO0865;
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SMART; SM00265;
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; Q07817; 1MAZ.
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                                                                                                                                                                                                                                                                                                                                                               GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
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Bcl2_BH4.
BCL2_family.
Bcl2_reg.
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BH3.
BH1.
BH2.
POTENTIAL.
POTENTIAL.
CLEAVAGE (BY CASPASE-3 AND PHOSPHORYLATION (BY PKC) (FOR PHOSPHORYLATION)
PHOSPHORYLATION (BY PKC) (FOR PHOSPHORYLATION)
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4; Mismatches
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Pred. No. 3
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(BH4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

TIGRFAMS; TIGR00865; bCl-2; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS0062; BCL2 FAMILY; 1.

APOPLOS18; Transmembrane.

DOMAIN 101 120 BH1.

DOMAIN 152 167 BH2.

TRANSMEM 181 198 POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJINE-95331613; PubMed=7607538;

CTUZ-Reyes J., Tata J.R.;

"Cloning, characterization and expression of two Xenopus bcl-2-like cell-survival genes.";

Gene 158:171-179(1995).
-!- FUNCTION: Confers strong protection against cell death.
-!- SUBCELULAR LOCATION: Membrane-bound (Potential).
-!- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the brain of mid-metamorphosic to post-metamorphosic tadpoles and adults, where an increase of several fold has been observed.
-!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
-!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000712; Bc12_BH.
InterPro; IPR003093; Bc12_BH4.
InterPro; IPR0032475; Bc12_family.
InterPro; IPR004725; Bc12_reg.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X82461; CAA57844.1; -. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the Bcl-2 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
[1]
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                                                                     184 RLLTI-VMLTGVFAL 197
                                                                                                                                        124 VESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFG
                                                                                                                                                                           108 AESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G 165
                                                                                                        166 NWASVRTVLŢĢAVĄL 180
                                                                                                                                                                                                                 64 EATESFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALC
                                                                                                                                                                                                                                                            4
8
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                                                                                                                                                                                                                                                    AAGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFEVEGAALC 107
                                                                                                                                                                                                                                                                                         SRDLVEKFVSKKLSO-NEACRKFSNNPNPMPYLMEPSTSERPGEGATOGIVEBEVLOALL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            moved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Result
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Maximum DB
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Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-155-327G-7
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2: pir2:*
3: pir3:*
4: pir4:*
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                                                              MATPASAPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193
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Bak protein - huma
gene bcl-xshort pr
cdn-2 protein - hu
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BCL-X-Long - rat
B-cell lymphoma 2
apoptosis regulato
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                   apoptosis suppress
bcl-2-associated p
Bax-delta protein
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bcl-2-associated p
protein ced-9 [imp
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BCL-X protein - ra
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A;Status: preliminary A;Molecule type: mRNA A;Residues; 1-233 «KAM» A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623 C;Superfamily: bcl apoptosis regulator, inhibitory type

RESULT 2 B47537

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141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183

NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL

66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124 29 CGAGPGEGPAAD------PLHQAWRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT

80 65 28 4

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Matches Query Match Best Local (

93; Conservative Similarity

42.6%; Score 428.5; DB 2; Length 233; 41.3%; Pred. No. 2.9e-32; tive 22; Mismatches 57; Indels 53

53;

Gaps

11 RALVADFVGYKLROKGY-------

RELVVDFLSYKLSOKGYSWSOFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV

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125

apoptosis regulator bcl-xL - human N; Alternate names: bcl-2-related p N; Contains: apoptosis regulator bc

d protein

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C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator
A;Reference number: A47537; MUID:93364977; PMID:8358789
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
551761
BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01
C;Accession: S51761; S51762
                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Moslecule type: DNA
A;Residues: 1-125,189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:g607176;
A;Experimental source: embryonic; brain
                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-233 <MIC>
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1;
A;Experimental source: embryonic; brain
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C;Superfamily: bcl apoptosis r
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A;Residues: 1-69,'G',71-125,189-233 <B02>
A;Cross-references: GB:L20122; NID:g623236;
                                            A; Introns: 125/3 C; Superfamily: b;
                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data A; Reference number: S51761 A; Accession: S51761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: BCL2L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
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A; Residues: 1-233 <BOI>
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                                                                                    A;Note: smaller form due C;Genetics:
                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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                                                                                                                                                                                                                                     Accession: S51762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
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                                              159
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                                          apoptosis regulator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%;
                                                                                                           to splicing
  42.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
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  Score
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Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                 November 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-Sep-1995 #text_change 28-Jul-2003
                                        inhibitory type
  424.5;
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                                                                                                                                                     PIDN: CAA57887.1;
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  233;
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C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993
C;Accession: A37332; S35453
R,Bguchi, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chic A;Reference number: A37332; MUID:92375724; PMID:150
A;Accession: A37332
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S
Blochim. Biophys. Acta 1132, 109-113, 1992
A;Title: Molecular cloning and DNA sequence
A;Reference number: 824390; MUID:92379084; F
A;Accession: $24390
                                                                                     transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S24390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: bcl apoptosis regulator, C; Keywords: mitochondrion; transforming
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A; Residues: 1-233 <EGU>
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92; Conserv
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                                                                                                                                                                                                                                                                                                                               ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                            DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAAAAAAAAGASSHHRPEPPGSA
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38.0%; Pre
vative 32;
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Pred. No. 8.3e-32;
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                                                                     S.; Reed,
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PMID:1511008
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PMID:1508712
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-58, 'T', 60-116, 'R', 118-239 < CLE>
A; Residues: 1-58, 'T', 60-116, 'R', 118-239 > CLE>
A; Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID
R; Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wri
Oncogene Res. 2, 263-275, 1988
A; Title: Consequences of the t(14;18) chromosomal translocation
A; Reference number: A27622; MUID:88217344; PMID:3285301
A; Accession: A27622
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSUS
A;Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PI
A;Note: this sequence has been corrected in reference A37332
A;Note: this sequence has been corrected in reference A37332
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett,
EMBO J. 7, 123-131, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-239 <EGU>
A;Note: this report is a correction
A;Note: this report is a correction
R;Tsujimoto, Y; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, a
A;Reference number: A29409; MUID:86259760; PMID:35
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C;Date: 31-Dec:1988 #sequence revision 07-Jun-1996 #text change C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
A; Molecule type: mRNA
A; Residues: 1-58, 'T', 60-239
                                                                                                                                                                                                                                 A; Title: Cloning and structural analysis of cDNAs for bA; Reference number: A24428; MUID:87002488; PMID:2875799 A; Accession: A24428
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A; Residues: 1-239 <SET>
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A;Title: Isolation and characterization of
A;Reference number: A37332; MUID:92375724;
A;Accession: C37332
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A;Residues: 1-232 <CAZ>
A;Cross-references: EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: mitochondrion; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTRALVADEVGYKLROKGYVCGAG-----PGEGPAADP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                         S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
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                                                                                                                                                                                                                                                                                                                         Sklar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shown;
                                                                                                                                                                                                                                                                                                                                                                                                                    somatic mutation; PMID:2834197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ripts, and protein PMID:3523487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the chicken bcl-2 gene: expression PMID:1508712
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                                                                                                                                                                                                                                                                                                                                                                                                                                       and deregulation
                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g179367
                                                                                                                                PID:g179371
Wright, J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.; Goldman,
                                                                                       in follicular lymphoma:
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                                                                                                                                                                                                                                                                          hybrid
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                                                                                                                                  Bakhshi,
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A; Cross-101C; Superfamily:
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A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487; PMID:7828536
A;Accession: 167432
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167432
                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: 167432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCL-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: blocks apoptosis in hematopoietic cells C;Superfamily: bcl apoptosis regulator, inhibitory type C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멍
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A;Map position: 18q21.3-18q21.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:BCL2
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL: U34964; NID: g1004378; PIDN: AAA77687.1;
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Best Local
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                                                                                                                                                                                                                                                          DTRALVADFVGYKLRQKGY----
                                   GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                        VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                              SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDNGGWDAFVELYG----PSMRPLFDFSWLSLXTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                              ----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNREIVMKYIHYKLSQRGYEWDÁGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART
                                                                       VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEFLVGQVQEWMVAYLETRLADWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLQTPAAPGAAAGPALSPVPEVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR
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36.2%;
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-PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                   regulator,
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                                                                                                                                                                                                                                                                                                           Score 412; DB 2;
Pred. No. 9.8e-31;
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                                                                                                                                                                                                                                                                                                                                                                   inhibitory type
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                                                                                                                                                                                                                                                                                            62;
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A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expre A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
TVMSA1
                                                                                                                                                                                                                                                                                                                                                                                                                           transforming protein bcl-2-alpha - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 31-Dec-1988 #seguence_revision 31-Dec-1988 #text_change 28-Jul-2003 C;Accession: A25960; E37332
                                                                                                                                                                                                                                                                                                                                                  Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression A;Reference number: A90893; MUID:87187643; PMID:3032455
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-236 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the
A;Reference number: IS3744; MUID:94193015; PMID:8144041
                                                                                                                                                      A;Residues: 1-33,
                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                            R; Negrini, M.;
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                                                                                                                      A;Gene: BCL2
                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-236 <NEG>
                                                                                                                                                                                                                                                                                                                                           A;Accession: A25960
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 Best Loc
Matches
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Best Local S
Matches 83
                                                                                                                                                                    Molecule type: DNA
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                                                                                                   ;Introns: 192/3
               Query Match
Best Local

    M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
455-463, 1987

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                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSOLHLTPFTARGRFAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VCGAGFGEGFAADFLHQAMRAAGDEFETRFRRTFSDLAAQLHVTFGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
                                                                                                                                                  'E',34-220,'AL',223-236 <EGU>
Conservative
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35.8%;
40.3%; Score 406; DB 1;
37.1%; Pred. No. 3.5e-30;
cive 33; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 407; DB 2;
Pred. No. 2.9e-30;
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                                                                                                                                                                                     not
                                                                                                                                                                                   shown;
                                                              transforming protein;
 61;
                                 Length 236;
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Indels
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                                                                                                                                                                                   compared
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52;
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                                                                                                                                                                                                                                      expression
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Gaps
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                                                                  transmembrane
                                                                                                                                                                                                                                                                                                                                                                          murine
                                                                                                                                                                                                                                                                                     PID: 9387109
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B-cell lymphoma 2 protein - Chinese hamster (Species: Cricetulus griseus (Chinese hamster) C;Species: Cricetulus griseus (Chinese hamster) C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 C;Accession: JC7383
R;Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000 A;Title: Cloning and functional analysis of cDNA en A;Reference number: JC7383

cDNA encoding

the

hamster

Bcl-2 protein

#text_change

28-Jul-2003

A;Cross-references: GB:AJ271720 C;Comment: This protein has ant C;Genetics:

has anti-apoptotic

function,

and

supports

cell survival

A; Molecule type: mRNA A; Residues: 1-236 < TOM>

A; Accession: JC7383 A; Contents: Ovary

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RESULT
JC7383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Tille: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: 153295; MUID:95129487; PMID:7828536
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A; Residues: 1-233 < RES >
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Superfamily: bcl apoptosis regulator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Rattus norvegicus (Norway rat);Date: 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                       185
                                                                                                        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
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                                                                                                                                                                        81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWWVAYLETRLADWIHS 140
                                                                                                                                                                                                                   66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE
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                                                                                                                                                                                                                                                       29 CGAGPGEGPAAD----
                                                                                                                                                                                                                                                                                                                               11 RALVADFVGYKLROKGY-----
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                                                                       NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                           RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNREIVMKYIHYKLSORGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART
                                                                                                                                            QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTRALVADFVGYKLROKGYVCGAG----
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EGPAADP-----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                                                    40.2%;
                                                                                                                                                                                                                                                     ---PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                    Score 404.5;
Pred. No. 4.8
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                                                                                                                                                                                                                                                                                                                                                                                    4.8e-30;
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bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-dul-1996 #sequence_revision
C;Accession: 149057
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C;Superfamily: bcl apoptosis re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C;Accession: A47537
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C;Superfamily: bcl
C;Keywords: B-cell
                                              R; Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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A; Accession: A47537
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A; Title: bcl-x,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                     I49057
                                                                                                                                                      RESULT
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. Immunol. 153, 4388-4398, 1994
;Title: Cloning and molecular characterization of mouse
;Reference number: I49055; MUID:95052604; PMID:7963517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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bcl-x, a bcl-2-related gene that f
bcl-x, a A47537; MUID:93364977;
                                                                                                                                                                                                     186
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Similarity 35.3%;
82; Conservative 3
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31; Conservative
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                                                                                                                                                                                                                                    EFTAL 150
                                                                                                                                                                                                                                                                     LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV
                                                                                                                                                                                                                                                                                                                                    VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                       RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNREIVMKYIHYKLSORGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                                                     LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                    -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%; Score 378; DB 2; Length 190; 43.8%; Pred. No. 1.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
egulator, inhibitory type
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Pred. No. 6.7e-30;
4; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                     02-Jul-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functions as ; PMID:8358789
                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
                                                                                 #text_change
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                 and T lymphocytes.
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   RESULT
B37332
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apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 28-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mclecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
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A;Residues: 1-227 <BAN>
A;Cross-references: GB:U72398;
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Similarity 40.8%;
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                              SGGWAEFTALYGDGALEEARR 161
                                                              QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184
                                                                                           QVSDELFQGGENWGRLVAFFVFGAALCAESVNKEWEELVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                            NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
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Pred. No. 2.3
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2.3e-27;
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Search completed: March 25, 2004, 15:45:06 Job time : 14 secs
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R;Equchi, Y: Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Status: nucleic acid sequence not shown
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A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl apoptosis regulator, inhibitory type
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C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text_change 28-Jul-2003
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Matches 71
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Local Similarity 38.4%; Pred. No. 1.4e-25;
hes 71; Conservative 21; Mismatches 49; Indels 44; Gaps
                                                                                                                                                                                               130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189
                                                                                                   190 VRACA 194
                                                                                                                                                    145 AEFTA 149
                                                                                                                                                                                                                                           85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                              70 AASEVPPAEGLRPAPPGVHLALROAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129
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   2004, 15:19:05; Search time 51 Seconds (without alignments)
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AAY69969
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Aaw9647 Human bcl
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Fragment

Bcl-Xl-DT

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ALIGNMENTS

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RESULT 1
AAYOSS30
ID AAYO
XX AAYO
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The present sequence is human Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AXX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules

ncluding genetic

sequences capable

of inducing,

enhancing or otherwise

Claim 2; Page 33; 52pp; English.

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RESULT 2
ADD46742
ID ADD44742
AC ADD4

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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                              The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially a more applied in a parisal exhibitor of the results.
                                                                                                                                                                                                                                                                                                               New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2002; 2002WO-US025765
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                        which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence
                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Woolf C,
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(FARB )
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ANK; Q92843.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pain; neuronal tissue; gene therapy; segmental nerve injury; chronic cons nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                             two or more isolated polypeptides, useful treating pain in an animal.
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Pred. No. 1.4e-102;
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        in neuronal tissue of a first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bcl-y protein
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Pred. No. 1
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Nucleic acids encoding B-cell lymphoma-y protein - unrecombinant protein for use in treating uncontrolled

useful

for growth

producing

1998-446079/38. DB; AAV28334.

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RESULT 4
AAW973
ID AAW9
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AC AAW9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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11-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999
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                                                                                                                                                                          Guastella
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                                                                                                                                                                                                                                             (COCE-)
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                                                                                                                                                                                                                                             COCENSYS INC.
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97US-00798897.
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Pred. No. 5e-102;
0; Mismatches
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WPI; 1999-214150/18. N-PSDB; AAX15946.

Novel bcl-y homologues

of the

rat and human bcl-2 protein - useful

for

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ARBSULT 5
AAW36047
ID AAW3
XX AAW3
AC AAW3
XX BC1-
XX Huma
XX Homo
XX YO97
XX YO97
XX O2-C
XX PB 27-M
XX YO97

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local S
                      Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 193 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bcl-w protein
                                                                                                                                                                                                                                                                               02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                           WO9735971-A1
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                                                                                                                                                                                                                   27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis;
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                                                                                           AMRAD OPERATIONS PTY LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic
inhibit
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protein associated with
                                                                                         animal model exhibiting reduced levels of a Bcl-w protein and/or
otein associated with Bcl-w.
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Disclosure; Page 37; 52pp; English

The present sequence is described of a derivative of human Bcl-w (see also AAY0533), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities and determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, can induce intertility enhancing or otherwise facilitating spermatogenesis inducing, ls, or which

Sequence 193 AA;

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              GALVTVGAFFASK 193
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GALVIVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     model.
                                                                                                                                                     HALL INST MEDICAL RES
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                                                                                  Gibson
                                                                                                                                                         WALTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse;
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                                                                                                                                                             ELIZA
                                                                              Koentgen
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WPI; 1999-243890/20

N-PSDB; AAX25133

animal model exhibiting reduced otein associated with Bcl-w.

levels

of a

Bcl-w protein

and/or

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RESULT 8
AAW97394
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Best Local Simi
Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see MAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological possess no other major abnormalities as determined by histological including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility
                                                                                                                                                                                    Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocarcial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                     Mammalian bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97394 standard; protein; 192
                                                    25-NOV-1997;
                                                                                       16-MAR-1999
                                                                                                                        US5883229-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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96US-0012201P.
97US-00798897.
                                                   97US-00978523.
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Pred. No. 8.
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3.3e-102;
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RESULT 9
AAW61391
ID AAW6
XX AAW6
XX AAW6
XX O2-O
DT O2-O
DE Rat
XX bcl-
XX bcl-
XX bcl-
XX US57
XX IS57
XX IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a mammalian bcy-1 protein. The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein (Lbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein chought to be involved in programmed cell death (appetbois and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death conhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular confidence of the selection, vitally induced cell death, aging, spinal cord injuries and confidence of the selection, vitally induced cell death, aging, spinal cord injuries and confidence of the selection where cells under go premature cell death as a result of triggers which may or may not be apparent. They can also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 191;
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Best Local
                                                                                                                                                                                                                                                                                                                        Rat bcl-y protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW61391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW61391 standard; protein; 193
                                                                                                                              US5789201-A
                                                                                                                                                                                                                                                         bcl-y; bcl-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                  cell death pathway; apoptotic; apoptosis; rat
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1.8e-101;
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RESULT 11
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Best Local S
Matches 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                           Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death;
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                                                                                                                                                                                                                            multiple screams; important amount probable sclerosis; cancer; aging; spinal cord life span; premature cell death; cell death stimulator; prolonged cell life span; promotive carrowns: lung cancer; autoimmune; hyperimmune disease; parasite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The rat bcl-y protein.
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Pred. No. 2.3e-101;
1; Mismatches 2;
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CC specification also describes human bcl-y protein (NDC1-y) and cpecification also describes human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of CC the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC - conditions where cells under go premature cell death as a result of CC - conditions where cells under go premature cell death as a result of CC injects which may or may not be apparent. They may also be used in this CC way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and CC Hbcl-y may be used to treat conditions associated with prolonged cell clife span such as cancer (especially kaposi's sarcoma and lung cancer) CC and auto/hyperimmune diseases. They may also be used to cause cell death con, and hence control, parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 15-18; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modulating programmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel bc1-y homologues of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX15945
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11-FEB-1997;
                                          Sequence 193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present seguence represents rat bcl-y protein (Rbcl-y).
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97US-00798897
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Length 193;
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                                                                                                                                                                                                            Similarity
                                                               QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                           FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                               FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
GALVTVGAFFASK 193
                        GALVIVGAFFASK 193
                                              QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                               MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                            98.9%;
98.4%;
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Pred. No. 2.3e-101;
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RESULT 11
AAW97393
ID AAW97397
XX AAW97
XX AAW97
XX Prote
XX Prote
XX Prote
XX Prote
XX Prote
XX Progr
KW Rat &
KW Progr
KW head
KW multti
KW aging
                                                                     Protein sequence of the specification.
                                                                                            20-MAY-1999
                                                                                                                                        AAW97393
                                                                                                                                        standard; protein;
                                                                                            (first entry)
                                                                                                                                          192
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Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; agoing; spinal cord injury; amyotrophic lateral sclerosis; cancer;

25-NOV-1997;

97US-00978523

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RESULT 12
AAY05533
ID AAY05
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AC AAY05
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DT 05-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 192 AA;
                                AAY05533;
                                                                 AAY05533 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.
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11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
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                                                                                                                                                  ALVIVGAFFASK 192
                                                                                                                                                                            ALVTVGAFFASK 193
                                                                                                                                                                                                                                               VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG
                                                                                                                                                                                                                                                                                  SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ
                                                                                                                                                                                                                                                                                                     SDLAAQLHVTPGSAQQRFTQVSDELFQGGENWGRLVAFFVFGAALCAESVNKEMEPLVGQ
                                                                                                                                                                                                                    VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG
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97US-00798897.
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                                                                 protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                   98.4%;
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Pred. No. 8.1e-101;
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05-JUL-1999

(first entry)

RESULT 13
AAW36048
ID AAW36
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AC AAW36

AAW36048 standard; protein;

AAW36048

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                                                                                                                                                                                                                                                                                                                                                                                The present sequence is described of a derivative of mouse Bcl-w (see called a hay05531), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The derivative lacks the 24 N-terminal amino acids of Bcl-w. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one generated the human or murine bol-w gene (see hAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which
                                                                                                                                                                                                                                                                     Matches 183;
                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                       Sequence 192 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-243890/20
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                                                                                                                                                      FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                        GALVTVGAFFASK 193
                                                                                    QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                   MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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GALVIVGAFFASK 192
                                                                QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL
                                                                                                                                 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                   Score 958.5; DB 2;
Pred. No. 3.1e-97;
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RESULT 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a novel protein, bcl-w, encoded by the mouse bcl -2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid
inhibit cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                    18-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cory s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1998
                                                                               AA018223
                                                                                                        AAO18223 standard;
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                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                161;
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                                                                                                                                                                                                                                                                                                     _
 apoptotic signal transduction
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                                                                                                                                                                                                QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
                                                                                                                                                                                                                                                                           MPTPASTPDTRALVADFVGYRLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                   MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                     QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA
                                                                                                                                                                                                                                                  FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      degenerative disease.
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding apoptosis related gene survival, e.g. for treatment of
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50-51; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96AU-00008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-AU000199
                                                                                                       protein; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gibson LM,
                                                                                                                                                                                                                                                                                                                                         86.1%;
95.8%;
                            domain
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                            related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLT
                                                                                                                                                                                                                                                                                                                                            Score 867; DB 2;
Pred. No. 3.3e-87;
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmgreen
                                                                                                        8
  protein; Bcl-Rambo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bcl-w - used to induce cancer and degenerative
                                                                                                                                                                                                                                                                                                                                                       Length 168;
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     BHNO
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    domain;
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RESULT 15 AAW59884 ID AAW59

AAW59884 standard; protein; 365

Amino 20-NOV-1998

acid

of the entry)

cDNA clone Bcl-like

(first

Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.

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                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of the human Bcl-Rambo apoptotic transcription factor, particularly the BHNo domain. The sequences are useful in the treatment of diseases caused by incorrectly regulated intracellular signal transduction, including cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's diseases), muscular dystrophy, viral infections (including human immunodeficiency virus), autoimmune disease, septic shock, graft versus host disease and acute hepatitis. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; neurodegenerative disease; Alzheimer's disease; cytostatic; nootropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory; immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock; Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2000; 2000DE-01061766.
04-JAN-2001; 2001DE-01000280.
                                                                                                                                                                                                                                                                                                                                           Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 6lpp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-537627/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200248353-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           graft versus host disease; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (APOT-) APOTECH RES & DEV LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-DEC-2001; 2001WO-EP014597
                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding Bcl-Rambo protein, useful for treating e.g. identifying therapeutic modulators of Bcl-Rambo function
178
                                 181
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                                                                                                                                                                                                      ۳
                                                                                                                                                                                                                                       1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                          Similarity
                                                                                          QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                      MATPASAPXTXAXVAD-XGYKLRQKGYVNGAGPGXGPAAD-XHQAXRAAGXEFETRFXRT
                                 GALVIVGAFFASK 193
                                                                                                                                    FSDLAAQLHVTPGSAQQRFTQVSDELFQGXPNWGXXXAFFVFGAAXCAESVNXEMEPLVG
 GALVTVGAFFASK 190
                                                                  QXQEXMVAYLETXLAX-IHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                        81.6%;
                                                                                                                                                                                                                                                                       Score 821.5; DB 5;
Pred. No. 4.1e-82;
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Homo sapiens

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Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies or tumours.
                                                                                                                                                                                                                                                                    Sequence 365 AA;
                                                                                                                                                                                                                                                                                                    can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV41925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-414099/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9831800-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC. (AUCK-) AUCKLAND UNISERVICES LTD.
                          121 QVQEWMVAYLETRLADWIHSSGGW 144
121
                                                                                       61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGBGPAADPLHQAMRAAGDBFETRFRRT 60
                                                                                                                                   1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Gentz RL, Feng P,
QVQEWMVAYLETRLADWIHSSGGW 144
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97US-0034205P.
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Search completed: March 25, 2004, 15:42:28 Job time: 52 secs

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Result
No.
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Listing first 45 summaries
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Perfect score:
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length: 2000000000
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                                                                                                                                                                                                       March 29, 2004, 04:18:04; Search time 2267.1 Seconds (without alignments) 7652.923 Million cell updates/sec
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AY421022
LOCUS
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  TITLE
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             2 (bases 1 to 582)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal,
Clark, A.G., Glanowski, S., Nielson, R., Tu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (Dases 1 to 582) (Dases, Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Kejariwal, A.,

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KEYWORDS
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This sequence as made by sequencing genor
                                                                            HTC; CAP trapper.
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs

[RL Nature 420, 563-573 (2002)]

RE Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojina, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Mishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Sakai, K., Sahich, S., Shibata, Y., Shibata, Y., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Szuzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Syshino, M., Muramatsu, M. and Hayashizaki, T., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp/) Fax:81-45-803-9216, Pax:81-45-803-9216, Intrinsical Research (South Riken.go.jp/) Tel:81-45-503-9222, Intrinsical Charles of Physical Course of South Riken.go.jp/) Tolibase visit our web site (http://genome.gsc.riken.go.jp/) for further details.
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 364 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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/db_xref="G1:12854053"
/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETRERRITESDLAAQLHVTPGSACQRETQVSDELFCGGPUNGRLVAFFVF
GAALCABSVNKEMEPLVGQVQDMYVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/clone_Tib="RIKEN full-length
/dev_stage="adult"
132._.713
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/db_xref="FANTOM_DB:4930488D08"
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18 6 (Dases 1 to 3487)

18 8 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Adachi, J., Pukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, F., Iayatsu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, X., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, The Institute of Characteristic Constitute of Cons
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yo
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) f
                                                                                                                                                               Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko
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Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
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Functional annotation of a full-length mouse Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                       Yokohama,
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COMMENT

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ORIGIN
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Best Local :
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                                                                                                          449
                                                                                                                                                                                   389
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361
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                                                                                                                                                                                                                                                                                                                                   269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
                                                                                                                                   CAGGTTTCCGACGACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                   AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC
                                                                                                                                                                                                                                                                                                                                                            AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC
 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                    GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
                                                                                                            CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                   TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                                                           CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                                                                           CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                            ATGGCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCGACCCCAGCCTCAACCCCCAGACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
                                      GTCTTTGGGGCTGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="lung"
/clone Tib="RIKEN full-length
/dev_stage="adult"
209. ..790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3487
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="bab23468.1"
/db_xref="01:12836028"
/translation="matpastpotralvadfvgyklrokgyvcgagpgegpaadplho
/translation="matpastpotralvadfvgyklrokgyvcgagpgegpaadplho
Amraagdefetrffreterbotlaaolhyvpgsaoorftoysdelfocgpnwgrlvaffvf
Gaalcaesvnkemeplvgovodwmvayletrladwihssggwaeftalygdgaleear
RLREGNWASTRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MGD | MGI : 108052)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C578L/6J"
/db_xref="FANTOM_DB:1200009L24"
/db_xref="MGI:1896837"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="unnamed protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="1200009L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 560.2; DB 11; Pred. No. 6e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product; Bcl2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3487;
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                                                                                                            508
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                                                                                                                                                                                                                                                                                                                                                                                                            268
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojina,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Yokohama, Kanagawa 230-0045, Japan

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AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                           NCE 1 (Ubases 1 to 369)

RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.M., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaii, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Pontius, J.U., Q.D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Q.D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Q.D., Ramachandran, S., Wells, C., Wang, Y., Taylor, M.S., Tesdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wang, Y., Watanabe, Y., Wang, L., Yasunishi, A., Yoshino, M., Waterston, R., Jawa, K., Shinaki, T., Waki, K., Kawai, J., Aizawa, K., Shinakaya, T., Konno, H., Nakamura, M., Sahakaya, T., Sakai, K., Sasaki, D., Shibata, K., Shinaki, Y., Sakai, K., Sasaki, D., Shibata, K., Shinaki, Y., Sakai, K., Sasaki, D., Shibata, K., Shinaki, Y., Sakai, K., Sasaki, D., Shibata, K., Shibata, Y., Sakai, Y., Watanasi, S., Lander, E.S., Shibata, Y., Sakai, Y., Watanasi, S., Lander, E.S., Shibata, Y., Sakai, Y., Sakai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
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BY715200 RIKEN full-length enriched, auu.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY715200.1 GI:27128317
EST.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 bp mRNA linear EST 17-DEC-2002
enriched, adult male testis Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                     372
                                                         241
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                                                                                                                                                                                                                                                                                                                                                  132
                                                                                                                                                                                                                                                                                                        61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                        μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (278) System--384-format Sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                           TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC
                                                                                                                                                                                                                            CCGCTGCAAGCCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCATTTTCCGCCGCACC
                                                                                                                                                                                                                                                                    AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC
                                                           CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                           ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sequences Mamm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              one="4930488D08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.1%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 558.6; DB 13; Pred. No. 8.8e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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  AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGAC 120
                                                             ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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                                                                                                                        Conservative
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/lab host="PH108 (phage-resistant)"
/lab host="PH108 (phage-resistant)"
/clone lib="NIH MGC 94"
/clone lib="NIH MGC 94"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6491566"
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96.8%;
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arrab	FEATURES source	AUTHORS TITLE JOURNAL COMMENT	AUTHORS TITLE JOURNAL PUBMED REFERENCE	VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 6 AY421020 LOCUS DEFINITION ACCESSION	QY db	gg V	dg Qy	Db Qy	D Qy	Qy Db	Qy 1	Qy Db	Db 1
	Hased OH allyHHELL. Location/Qualifiers 1582 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	lark, A.G., Glamodd, M.A., Tannodd, M.A., Tannodd, S., W. dams, M.D. and direct Submiss. ubmitted (16-1) ockville, MD. ockville, MD.	ეთ. ⊢1	AY421020.1 GI:39776977 GSS. Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo. Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.	in</td <td>537 ACTGGGGGCCCTGGTAACTGT-AGGGGCCTTTTTTGCTAGCAAGTG 581 </td> <td>478 CGGCGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGAC-GGGGGCCGTGGC 536 </td> <td>420 CAGT-GGCGGCTGGGCGGACTTCACAGCTCTATACGGGGAC-GGGGCCCTGGAGGACGCA 477 </td> <td>361 CAAGTCCAGGATTGGATCGTCGCCTA-CCTGGAGACACGTCTGGCTGACTGGATCCACAG 419 </td> <td>301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAATGGAGCCTTTGGTGGGA 360 </td> <td></td> <td>181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240 </td> <td>121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180 </td> <td> </td>	537 ACTGGGGGCCCTGGTAACTGT-AGGGGCCTTTTTTGCTAGCAAGTG 581	478 CGGCGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGAC-GGGGGCCGTGGC 536	420 CAGT-GGCGGCTGGGCGGACTTCACAGCTCTATACGGGGAC-GGGGCCCTGGAGGACGCA 477	361 CAAGTCCAGGATTGGATCGTCGCCTA-CCTGGAGACACGTCTGGCTGACTGGATCCACAG 419 	301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAATGGAGCCTTTGGTGGGA 360 		181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240	121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180	
	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the	CHGANISM HOMO SEDIERS ENLARYOTE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERRICE 1 (bases 1 to 804) AUTHORS Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. TITLE EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.) JOURNAL Unpublished (1999) COMMENT CONTACT: MIPS MIPS MIPS	- 6 5	541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581	4 4 4	Qy 361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420	301 301	Qy 241 CAGGITICCGACGAACTITICCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300	Qy 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCTCAGCCTCACC 240	Qy 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGTTTCCGGCGGACC 180 Db 121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATTAGAGACCCGCTTCCGGCGCACC 180	QY 61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCTGGGGAAGGCCCAGCCGAC 120	Qy 1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60	Query Match 86.2%; Score 501; DB 29; Length 582; Best Local Similarity 91.4%; Pred. No. 3.7e-117; Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;	/gene="BCL2L2" /locus_tag="HCM7418"

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No s1 sequence available.

This clone (DKFZp761D0816) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
 Homo
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                                                                                                                                                                                                            GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF7p761D8916"
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/dev_stage="adult"
/lab_host="MHOB"
/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sa
                                              GI:10214832
              (human)
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Pred. No. 4.1e-111;
0; Mismatches 50;
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                                                                                          cDNA clone IMAGE:3944307
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                AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCCTGGAGGAGGCGCGG
                                           AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGCCCTGGAGGACGCACGG
                                                                                                                                         GTCTTTGGGGCTGCACTGTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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300 383

623 480 563 420 240

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.g
Plate: LLCM800 row: p column: 04
High quality sequence start: 5
High quality sequence stop: 709.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the collections of the
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                                                                                                                                                                                                                                                                                                              /lab host="UH10B (phage-resistant)"
/clome lib="NHIMGC_7"
/clome=Torgan: lung; Vector: pCTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Lim Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:3944307"
/tissue_type="small cell
/cell_line="MGC3"
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/db_xref="taxon:9606"
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                                                            82.1%;
Score 477; DB Pred. No. 6.5e. 0; Mismatches
                                                            477; DB 10;
No. 6.5e-111;
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Hominidae; Homo.
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Best Local S
Matches 520
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Email: cgapbs-rGmail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9853 row: h column: 07
High quality sequence start: 3
High quality sequence stop: 650.
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5', mRNA sequence.
EF785386
EF785386.1 GI:12090422
EST.
Mus musculus (house mouse)
Mus musculus (house mouse)
Rnike-concernic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 815)
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National Institutes of Health,
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                                                            GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCGACGAACTTTT
                                                                                                                GGCTGCTGGAGACGAG-TTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                           TGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGGCCGACCCGCTGCACCAAGCCATGCG
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     CCAAGGGGGCCCTAACTGGGGCCCTTGTGGCATTCTTTTGTCTTTTGGGGCCTGCCCTGTG
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/dlone="IMAGE:4239798"
/dlone="IMAGE:4239798"
/lab_host="MH108 (T1 phage-resistant)"
/clone_lib="NCI CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library. | "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain="FVB/N"
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1.1e-98;
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                                                                                                                                                                   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,X., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
The FANTOM Consortium and the Group Phase I & II Team.
Analysis of the mouse transcri
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AK013244
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Mus musculus 10, 1
enriched library,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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11 days embryo whole body cDNA, RIKEN full-length
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     transcriptome based
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2 6 (bases 1 to 854)

S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carrinci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayarsu, N., Hiramoto, K., Hiramota, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyaraki, A., Nishi, K., Nomura, K., Nimazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                           196 ATGGCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 255
        61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
                                                                                         1 ATGCCGACCCCAGCCTCAACCCCAGACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-UU-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Host: SOLR
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                /protein_id="Bab28740.1"
/db_xref="G1:12850488"
/db_xref="G1:12850488"
/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGFGEGPAADFLHQ
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GAALCAESVNKEMEFLVGQVQDMWVAYLETRLADWIHSSGGWVRSSQLLLSASLYKVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                  LHGKIGPLMGGWGCAGRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MGD | MGI: 108052)
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_xref="MGI:1902183"
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Pred. No. 7.6e-97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 21
High quality sequence stop: 695
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11526 row: k column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

[bases 1 to 697]
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                                                                                                                               /lab_host="DH10B"
/clone lib="NIH MGC 122"
/clone lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5209862"
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             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                            Mammalla; Eutheria; Rodentia; Craniata; Mammalla; Eutheria; Rodentia; Sciurognati (bases 1 to 792)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                     BG298789 792 bp r
602396527F1 NIH_MGC_94 Mus musculus
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Mus musculus (house mouse)
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              1 (bases 1 to 623)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                          623 bp
AMGNNUC:NRDG1-00100-H10-A nrdg1
clone nrdg1-00100-h10 5', mRNA s
CB578463
CB578463.1 GI:29522504
EST
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High quality sequence stop:
Location/Qualifiers
                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            Rattus norvegicus (Norway Rattus norvegicus
                                                                                 Rattus.
 Contact: Dan Fitzpatrick
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/db_Xref="taxon:10090"
/db_Xref="taxon:10090"
/clone="IMAGE:45:11215"
/tissue_type="retina"
/lab_Most="DH10B (phage-resistant)"
/lab_Most="DH10B (phage-resistant)"
/clone lib="NH1 MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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One Amgen C
Tel: 805 44
Plate: 0010
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,'Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., SchuRitter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCan Waterston,R. and Wilson,R.
                                                                                                                                                                              AW258810
540 bp mRNA linear EST 23-DEC-1999 um74a02.y1 Sugano mouse kidney mkia Mus musculius cDNA clone IMAGE:2300906-5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS REGULATOR BCL-W. [2] SW:BCLW_MOUSE j, mRNA sequence.
AW258810
AW258810
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                                                                                                  Eukaryota;
Mammalia; |
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/clone_Tib="nrdg1 (10855)"
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                                                                                                  Eutheria;
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JOURNAL
                                                                                                                                                                                                                                                                                                                                    source
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MGI:1009678
Seq primer: custom primer used
High quality sequence stop: 467
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
/organism="Mus musculus"
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                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                                                                                                                                                                                 /dev_stage="adult"
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Query Match Best Local Simi Matches 420; Local Similarity 472 361 412 301 352 241 292 181 232 121 172 112 61 \vdash CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360 CCGCTGCAAGCCAAGCGAGCTGCTGGAGAGACGAGTTTGAGACCCGTTTCCGCCGCACC AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGGAAGGCCCAGCCGCCGAC ATGGCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGGCTGACTTTGTAGGCTAT CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGGCCGTCTTGTGGCATTCTTT CAGGITTCCGACGAACTITTCCAAGGGGGCCCTAACTGGGGCCCGTCTTGTGGCATTCTTT AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAAGGCCCAGCCGGAC TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC Conservative 69.5%; 0 Score 403.6; DB 1 Pred. No. 2.8e-92; Mismatches DB 10; 9 Indels Length 540; <u>ب</u> Gaps 471 411 300 351 240 291 180 231 120 171 60 <u>بـ</u>ــ

AGTGGCGGCT

Q Y	Db			νΩ V	Query Match Best Local Matches 40	ORIGIN	BOUTCE	FEATURES					COMMENT	MEDLINE	JOURNAL	BTLLE	ACTRONS	REFERENCE		ORGANISM	KEYWORDS	ACCESSION VERSION		DEFINITION	CA391923
121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACCGAGTTTGAGACCCGTTTCCGCCGCACC 180	235 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 294	AGGCTGAGGCAGAAGGGTTAIGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC 1	argacaaccccaaccrcagccccaaacacacacgccragacgcagacrrrgraggrar 2	recceaccccaecctcaj	Simil 8; (NIT INCIAMOTAL SEQUENCING CENTER (NISC).	/organism="Homo sapiens"	Location/Qualifier	Plate: 20 row: C column: 09 Plate: 20 row: C column: 09 Seg primer: M13RP1 reverse primer (ABI).	Fax: 301 496 00716 Fax: 301 496 00716 Fax: 301 496 00716	Macticiat by Carifornia (1989) 1984 (1984)	Section on Molecular Structure and Function	12107410 Contact: Wistow G		and splice variants Mol. Vis. 8 (4), 205-220 (2002)	ressed sequence tag analysis of numan Bank Project: Over 6000 non-redundant	ard, G., Smith, D. and Peterson, K.	Hornatoin of Wratt M V Carrie o N Dahal	uka	Homo sapiens	Ś	CA391923 CA391923.1 GI:24724221	èquence. .zeu, unampritteu/: ca nomo aaprena coma crona	1 Human Retinal pigment epithelium/choroid cDNA	mRNA linear

Search completed: March 29, 2004, 07:28:10 Job time : 2269.1 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX022531	RESULT 1
apoptosis-controlling genes Patent: EP 0932674-A 8 04-AUG-1999;	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of	Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.		unclassified.	unidentified ,	unidentified		AX022531.1 GI:10046127	AX022531	Sequence 8 from Patent EP0932674.	AX022531 581 bp DNA linear PAT 07-SEP-2000		

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                                           AX030819 581 bp
Sequence 8 from Patent W09735971.
AX030819
AX030819.1 GI:10278313
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Patent: WO 9735971-A 8 02-0CT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU);
GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
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582 bp (bcl-w) mRNA,

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'db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome="14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _line="BaF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; I
Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 560.2; DB 10;
Pred. No. 5e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell survival; Bcl-2 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bernard, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copeland, N.G., and Cory, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell survival
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DEFINITION
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AUTHORS
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VERSION
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Mus musculus BCL-W (Bcl-w) mRNA,
AF030769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-OCT-1997) Center University, 1462 Clifton Road, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3476)
Ross, A.J. and MacGregor, G.R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-w is required for testis homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ross,A.J., Waymire,K.G., Moss,J.E., MacGregor,G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF030769.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       npublished
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                                                                                                                                                        /product="BCL-w"
/protein_id="AAB86430.1"
/protein_id="AAB86430.1"
/db_xref="GI:250"
/translat.on="VATPASTPDTRALVADFVGYKLRQKGYVCGAGPGBGPAADPLHQ
/translat.on="VATPASTPDTRALVADFVGYKLRQKGYVCGAGPGBGPAADPLHQ
AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                      /note="mRNA destabilization 3428. .3441
                                                                                                                                         RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                83. .170
                                                                                                                                                                                                                                                                                                           /gene="Bcl-w"
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Bcl-w"
                                                    356. .3364
/gene="Bcl-w"
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codon_start=1
                                                                                                                                                                                                                                                                                             179. .760
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/number=2
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/number=1
                                                                                                      gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               map="19.5 cM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain="C57BL/10J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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complete
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                                       element"
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Best Local :
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           Hamner,S., Skoglosa,Y. and Lindholm,D.
Direct Submission
Submitted (01-007-1998) Developmental Neuroscience, Uppsala
University, Box 587, EMC, Uppsala 751 23, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGAC
                                                                                                                                                             1 (bases 1 to 582)

Hammer, S., Skoglosa, Y. and Lindholm, D.

Differential expression of bcl-w and bcl-x messenger developing and adult rat nervous system expression of bcl-w and bcl-x messenger developing and adult rat nervous system
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                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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AF096291
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                                                                                                                                                                                                                                                        Rattus.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                  AF096291.1 GI:3747129
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                                                                                                        (bases 1 to 582)
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                                                                                                                                                                                                                                                                       Chordata; Rodentia;
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Pred. No. 3.8
                                                                                                                                                                                                                                                                                                                                                                                                    582 bp
(bcl-w)
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ches 13;
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Nete cds.
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               Rattus norvegicus BCL-WEL mRNA,
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GAALCAESVNKEMEPLVGQVDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/mol type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:1016"
/tissue_type="brain"
/tissue_type="brain"
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0; Mismatches 23;
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Blvd., Philadelphia, PA 19104, USA
Location/Oualifice
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Itoh, T., Itoh, A. and Pleasure, D.
Bcl-2-related protein family gene exproligodendrogical differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
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Mammalia; Eutheria;
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Similarity 96.0%;
58; Conservative
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  CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGGCCGTGGCACTG
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                          CAGGTTTTCCGACGACGTTTTCCAAGGGGGCCCCTAACTGGGGCCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                   CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                                                                                                       TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC
                                                                                                                                                                                                                                                                                                                       AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGGAAGGCCCAGCCGAC
                                                                                                                                                                                                                                                                          AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC
                                                                                                                                                                                                                                                                                                                                                                    ATGGCGACCCCAGCCTCAACCCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT
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Mismatches

23;

Indels

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3487
Rattus norvegicus BCL-W mRNA,
AY185098
AY185098.1 GI:321852A0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 3487) Itoh, T., Itoh, A. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Itoh, T., Itch, A. and Pleasure, D.
Bcl-2-related protein family gene expr
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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vd., Philadelphia, PA 19104, USA
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                                                                                  /translation="WATPASTPDTRALVADFVGYKLRQKGYVCGAGFGEGPAADFLHQ
AMRAAGDFFERRFTSDLAAQLHVTFGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNEMBEJLVGQVQDMYVTYLETRLADWIHSSGGWABFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                    /protein_id="AA064468.1"
/db_xref="GI:32185281"
                                                                                                                                                                                                          /product="BCL-W"
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                                                                                                                                                                                                                             codon_start=1
93.7%;
96.0%;
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Rodentia;
Score 544.2; DB 10; Pred. No. 2.1e-117;
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Sciurognathi;
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thi; Muridae; Murinae;
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Direct Submission
Direct Submission
Submitted (29-OCT-2002) Biotechnology, P
                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (22-SEP-2003) Biotechnology, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mis musculus Bcl2-like protein 2 mRNA, complete cds. AY170344
AY170344.2 GI:34857712
                                                                                                                                                                                                                                                                                                                       Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan Sequence update by submitter On Sep 22, 2003 this sequence version replaced gi:27497698 Location/Qualifiers
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3 (bases 1 to
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Mammalia; Eutheria;
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Mus musculus
               Similarity
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93.1%;
ilarity 95.7%;
Conservative
                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10000"
/tissue_type="skin"
/dev_stage="neonatal"
/note="isolated after IGF-
                                                               /codon_start=1
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/protein_id="AAO13177.2"
/db_xref="G1:34857713"
/db_xref="G1:34857713"
/translation="MATPASTPDTRALVAYFVGYQLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDELQTERFRT#SSHLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKHMEPLVGQVQDWNVAYLETRLAYWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFAYK"
                                                                                                                                                                                         /note="c98; Bcl2-c98"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nei-Pu Hsiang, 3473)
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Rodentia;
Score 541; DB
Pred. No. 1.2e-
0; Mismatches
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.2e-116;
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Sequence
AR020779
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Guastella,J.
Genes coding for bcl-y a bcl-2 homologue
Patent: US 5789201-A 1 04-AUG-1998;
Location/Qualifiers
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                                                                           ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
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/mol_type="unassigned
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                                                                                                                  Score 540.6; DB 6;
Pred. No. 2e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                  AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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1 (bases 1 to 582)

Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival oncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                               Submitted (03-JUN-1996) Molecular Biology Unit, The
Eliza Hall Institute of Medical Research, PO Royal
Hospital, Parkville, Victoria 3050, Australia
Location/Qualifiers
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US9747
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                                                                                             /gene="bcl-w"
/note="promotes (
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GAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                                                                                                                                                        /gene="bcl-w"
                                                                                                                                                                           /map="14q11"
1. .582
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/mol_type="mRNA"
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                                                                                        Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human ger The coding sequences of 80 new genes (KIAA0201-KIAA0280) ded analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
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2 (bases 1 to 3542)
Ohara,O., Nagase,T., Kikuno,R. and
Direct Submission
Submitted (27-AUG-1996) Osamu Ohara
1532-3, Yana, Kisarazu, Chiba 292-0
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/tissue type="brain"
/clone Tib="psport 1"
1. .3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="baa19666.1"
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GaalcaesvnkemeplvgQvoewmvaylettrladwihssggwafftalygdgaleear
Rlregnwasvrtvltgavalgalvtvgaffask"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="KIAA0271"
/note="similar to
(A24428)"
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177. .758
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/db_xref="taxon:9606"
/clone="HA6752"
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Pred. No. 1.3e-107;
0; Mismatches 49;
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                                                                CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGGCCGTGGCACTG
                                                                                                                    AGTGGCGGCTGGGCCGACTTCACAGCTCTATACGGGGACGGGGGCCCTGGAGGACGACGG
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                                                                                                                                                                                                CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                                                                                                                                                                                                       GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA
                                                                                                                                                                                                                                                                                                                        CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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GGGGCCCTGGTAACTGTAGGGGGCCTTTTTTGCTAGCAAGTG
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/db_xref="G1:10046126"
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/mol_type="unassigned DNA"
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Pred. No. 4e-107;
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A novel mammalian gene, bcl-w, belongs to t
apoptosis-controlling genes
Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P
GIBSON LEONIE M (AU); AMRAD OPERATIONS P
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                                                                                     CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                                                                                                      GICTTTGGGGCTGCCCTGTGTGCTGAGAGAGTGTCAACAAAGAAAIGGAGCCTTTGGTGGGA
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Pred. No. 4e-107;
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481 CGTCTGCGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540	Db
481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTG 540	VQ
421 AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCGCGG 480	DЬ
421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGCGCCCTGGAGGACGCACGG 480	9
361 CAAGTGCAGGAGGGTGGTCGTCGTGGAGACGCGGCTGGCT	Дb
361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420	VΩ
301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360	Db :
301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGAGTGTCAACAAAGAAATGGAGCCTTTTGGTGGA 360	Qy
241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGGCCGCCTTGTAGCCCTTCTTT 300	ga
241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300	Qy
181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240	Dβ
181 TICTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAGCAACGCTTCACC 240	γQ
121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATTCGAGACCCGCTTCCGGCGCACC 180	ф
121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180	QY
61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120	Дb
61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGCAAGGCCCAGCCGCCGAC 120	9
1 ATGGCGACCCCAGCCCCCAGACACACGGCTCTGGTGGAAGACTTTGTAGGTTAT 60	дb
1 ATGCCGACCCCAGGCCTCAGCCCCAGACACACGCGCTCTAGTGGCTGACTTTTGTAGGCTAT 60	Qy
ery Match 85.6%; Score 497.4; DB 6; Length 579; est Local Similarity 91.2%; Pred. No. 2.8e-106; atches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;	5 T
/mol_type="unassigned DNA" /mol_type="unassigned DNA"	ORIGIN
L Patent: US 5789201-A 2 04-AUG-1 Location/Qualifiers 1. 579 / Transfer Patent Patent	JOURNA FEATURES Sou
I (bases 1 to 5/9) Guastella, J. Genes coding for bcl-y a bcl-2 hom	REFERENCE AUTHORS TITLE
Unknown. SM Unknown. Unclassified.	
Sequence 2 from patent US 5789 AR020780 AR020780.1 GI:3975395	DEFINITION ACCESSION VERSION KEYWORDS
LT 15 0780 S AR020780 579 bp	80
541 GGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581	DЬ
541 GGGGCCCTGGTAACTGTAGGGGGCCTTTTTTGCTAGCAAGTG 581	Qy
481 CGTCTGCGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCGCGCGC	DЪ
481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540	γQ

Search completed: March 29, 2004, 06:11:59 Job time : 2757.26 secs

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Aax25135 Mouse bcl
Aax25135 Mouse bcl
Aax25135 Mouse bcl
Aab52996 Primary r
Aav28333 Rat bcl-y
Aax15945 CDNA enco
Abv78153 Human bcl
Abx35729 Human bcl
Abb191694 Human bcl
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Aax25132 Human bcl
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Aax2636 CDNA enco
Aav41925 Nucleotid
Aav59630 Human cDN
Acx15946 CDNA sequ
Abs73617 Human imm
Abi3229 Human imm
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ALIGNMENTS

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RESULT 1
AAT96578
CDS
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                                                                                                                                                             Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; ss.
                                                                                                                                                                            Mouse bcl-w DNA.
                                                                                                                                                                                               AAT96578;
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                                                                                                                                                                                     22-APR-1998
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/*tag= a

/product= "bcl-w"

/note= "q"
                                                                                                                                           Location/Qualifiers
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Cory (AMRA-) 5 AMRAD OPERATIONS PTY LTD. Adams JM, Gibson LM,

27-MAR-1996;

96AU-00008965 97WO-AU000199

27-MAR-1997;

Holmgreen SP;

WPI; 1997-489635/45. P-PSDB; AAW36048.

Nucleic acid encoding inhibit cell survival, diseases. apoptosis related gene e.g. for treatment of cancer and degenerative bcl-w used to induce or

Claim 3; Page 50-51; 86pp; English.

This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,

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                                                                                                  05-JUL-1999
                                                          Spermatogenesis; animal model; ss
                                                                                   Mouse bcl-w gene
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                                                                  Bcl-2; mouse; fertility; infertility;
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Pred. No. 6e-148;
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The present sequence is described as a derivative of the mouse bol-w gene (see AAX25133) and encodes Bol-w protein (see AAX05533), a pro-survival member of the Bol-2 family which is widely expressed and which is cessential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of the molecules and generic sequences useful for inducing or reducing fertility, of male animals. Methods are provided for the treatment of infertility, of male animals. Methods are provided for the treatment of infertility, or of reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol-w gene or in a gene associated with bol-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis or in animals, or which can induce infertility
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BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

Similarity CAGGITTCCGACGACGTTTTCCAAGGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGGA CCGCTGCACCAAGCCATGCGGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAAGGCCCAGCCGCCGAC ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT Conservative 100.0%; 0 Score 581; DB 2. Pred. No. 6e-148); Mismatches (2 <u>.</u> Length 581; Indels 0 Gaps 240 480 420 360 360 300 180 120 60 60 420 300 240 180 120

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                                                                                                                                   Similarity
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                                      ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG
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                                                                                                              Score 560.2; DB 2;
Pred. No. 2.7e-142;
0; Mismatches 13;
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                                                                                                                                                                      AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG
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RESULT 4 ADB52996 ADB52996 standard; DNA; 582

ВP

ADB52996;

04-DEC-2003

(first entry)

Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.

primary toxicity marker; toxic effect; gene expression profile; hepatotoxicity; rat hepatocyte toxicity toxicity modelling; gene; ds progression; drug screening; diagnostic marker;

Rattus norvegicus

WO2003065993-A2

14-AUG-2003

13-MAR-2002 08-APR-2002 10-APR-2002 110-APR-2002 110-APR-2002 110-APR-2002 110-APR-2002 110-APR-2002 110-APR-2002 120-APR-2002 120-APR-2002 120-APR-2002 120-MAY-2002 120-MAY-2002 120-MAY-2002 120-MAY-2002 120-MAY-2002 04-FEB-2003; 2002US-0363534P 2002US-0370248P 2003WO-US003482

2002US-0371134P.
2002US-0371135P.
2002US-0371139P.
2002US-0373601P.
2002US-0374139P.
2002US-0374139P.
2002US-0378370P.
2002US-0378653P.
2002US-0378665P.
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AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGAC

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Best Local Similarity
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04-SEP-2002;
28-JAN-2003;
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CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCCTGGCACTG
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; 2002US-0407688P.
; 2003US-0442900P.
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Pred. No. 6.1e-138;
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                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                 The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding B-cell lymphoma-y protein - useful for recombinant protein for use in treating uncontrolled cell grov
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/note= "No stop codon given"
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                                                                                                                                                                                                                                                                                                                      C; 198 G; 113
                                                                                                                                                                                                             Score 540.6; DB 2;
Pred. No. 5.8e-137;
0; Mismatches 24;
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            Disclosure; Col 13-16; 26pp; English
                                                                        WPI; 1999-214150/18
P-PSDB; AAW97391.
                                                                                                            Guastella
                                                                                                                                                          23-FEB-1996;
11-FEB-1997;
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RESULT 7
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ABV78153;

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Pred. No. 5.8e-137;
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Query Match
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Matches 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overhang of 1-4 nuclectides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a gene related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2001;
29-NOV-2001;
07-DEC-2001;
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 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
                           GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
                                                                                                                      TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    C; 211 G; 111
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Pred. No. 1.7e-127;
0; Mismatches 47;
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                                                        The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonuclectides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours or infections, especially by plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; viru protozoacide; gene expression; antisense; tumour; infection; Plasm virus; viroid; anti-GPP; human; HIV; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; human papilloma virus; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 30-31; 100pp; German.
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RESULT 9
ABXO9972
ID ABXO
XX ABXO
XX ABXO
XX ABXO
XX Olig
KW Pric
XX Ponc
XX Ponc
XX Olig
KW Pric
XX Ponc
XX Ponc
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XX All
XX ABXO
XX AB
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                                                                                                                                                                                                                                                                                                                                                   Oligoribonucleotide;
                                                           Kreutzer R,
                                                                                                                                                                         09-JAN-2001; 2001DE-01000587.
                                                                                                                                                                                                                  21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                  (RIBO-) RIBOPHARMA
                       2002-742209/81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CETCTECEGEAGECCAACTEGECATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTG
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0; Mismatches 47;
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                                                           Hadwiger
                                                                                                                                                                                                                                                                                                                                                   cytokine;
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밁 Š 밁 S В δõ 밁 5 밁 S Дb

> Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, treating the cell with interferon. ş after

35-36; 98pp; German

target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes; developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene a least one oligoribonuclectide (dsRNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nuclectides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsNNAI. The method is used to inhibit expression of ם

Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

87.1%; 91.9%;

Score 505.8; DB 6; Pred. No. 1.7e-127;

Length

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ATGCCGACCCCAGCCTCAACCCCCAGACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT ccecrecaccaaeccareceeecrecaeaeaccaerrreaeacccerrrcceccecacc AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAAGGCCCAGCCGAC GGGGCCCTGGTAACTGTAGGGGCCCTTTTTTGCTAGCAAGTG CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGGCCGTGGCACTG AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC ATGGCGACCCCAGCCTCGGCCCCAGACACACGGCTCTGGTGGCAGACTTTGTAGGTTAT TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC Conservative IGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 0; Pred. No. 1.70); Mismatches 47; Indels 581 581 0 Gaps 540 60 60 480 480 420 420 360 360 300 300 240 240 180 180 120 120

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ABL91694;

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Best Local S
Matches 534
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for inhibiting expression of a target gene (ABL91659-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; HIV;
Plasmodium;
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                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting gene expression introducing double-stranded
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                                                                                                                                                                                                                                                                                                                                                                                                        increases stability and thus intracellular concentration
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301
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                                                                                                                                                                                                                                                                                                                                   Similarity
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 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
                                            CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                               AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                                                                                                        ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
                                                                                                                                                                                                                                                                                 ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                                                     CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                                                        CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV; gene expression; oligoribonucleotide; tumour; pathogen; virus; viroid; cytokine; prion; antisense oligonucleotide; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Limmer S,
                                                                                                                                                                                                                                                                                                                   Conservative
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91.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in cells, useful for e.g. treating tumors, d complementary oligoRNA having unpaired
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                                                                                                                                                                                                                                                                                                                 Score 505.8; DB 6;
Pred. No. 1.7e-127;
D; Mismatches 47;
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                                                                                                                                                                                                                                                                                                                                                                             T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                   Indels
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RESULT 11
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                                                                            The present sequence is the human bol-w gene encoding Bol-w protein (see AAY05530), a pro-survival member of the Bol-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol-w gene or in a gene associated with bol -w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An animal model exhibiting reduced protein associated with Bcl-w.
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                                                                               07-JUN-2002;
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Pred. No. 1.2e-126;
0; Mismatches 49;
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Novel DNAzyme useful for treating tumors, and for enhancing the sensitivity of malignant or virus infected cells to therapy, corcatalytic domain and binding domain contiguous to the catalytic comprises domain. a

Disclosure; Page 44-45; 67pp; English

The invention relates to a DNAzyme which specifically cleaves mRNA transcribed from a member of the bcl-2 gene family. The DNAzymes comprise a catalytic domain, binding domains contiguous with the 5' and 3' end of the catalytic domain, and therefore hybridise with, the two regions immediately flanking the purine residue of the cleavage site within the bcl-2 gene family mRNA, at which DNAzyme-catalysed cleavage is desired. A pharmaceutical composition comprising a DNAzyme of the invention is useful for treating tumours in a subject, and for enhancing the sensitivity of malignant or virus infected cells infected cells to therapy. The DNAzymes are useful in diagnostics, therapeutics, prophylaxis, research agents and in kits. The DNAzymes are also useful for increasing the susceptibility of tumour cells to anti-tumour therapes such as chemotherapy and radiation therapy. This polynucleotide sequence represents a human bcl-2 gene of the invention

Sequence 3542 ВP, 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Similarity

91.6%;

5; DB 7; 2.1e-126;

Length 3542;

δ В Ś Ś 밁 8 밁 맑 Ş 맑 S 片 S 밁 Š 멼 Ş 밁 Š Query Match Best Local Simi Matches 532; 717 657 597 537 361 477 417 357 481 421 301 241 181 297 121 237 177 61 _ GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCCAGCAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCTGGGGAAAGGCCCAGCCGCCGAC CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGGCCGTGGCACTG AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCCGCCTTGTAGCCTTCTTT TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC ATGGCGACCCCAGCCTCGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGGTTAT ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT Conservative ; Score 502.6; ; Pred. No. 2.1e 0; Mismatches 49; Indels 757 0 540 656 480 420 360 476 300 416 356 180 296 120 236 60 536 240 0

RESULT 13
AAT96577
ID AAT96
XX AAT96577 standard; DNA; 583 ВP

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                                                                                                                                                                                                                                                                             This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production
                                                                                                                                                                                                                                                Sequence 583
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 48; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW36047.
CAGGTITCCGACGAACTITTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                        CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                          ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams JM,
                                                                                                                     AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                        AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGAC
                                                                                                                                                              ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
                                                     TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                           CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ptosis; bcl-2; cell sur
degenerative disease;
                                                                                                                                                                                                     86.2%;
nilarity 91.4%;
Conservative
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                                                                                                                                                                                                                                                                     potential modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibson LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell survival; treatment;
                                                                                                                                                                                                        0
                                                                                                                                                                                                       Score 501; DB 2; I
Pred. No. 3.4e-126;
D; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmgreen
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                                                                                                                                                                                                                                                U; 0 Other;
                                                                                                                                                                                                                           Length 583;
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                                                                                standard; DNA; 583
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Human bcl-w gene derivative Spermatogenesis; bcl-3

gene; Bcl-2; human; fertility; infertility;

WO9913710-A1 Homo sapiens.

25-MAR-1999

16-SEP-1998; 98WO-AU000764

16-SEP-1997; 97AU-00009228

620 (HALL-) HALL INST MEDICAL RES WALTER & ß Adams J, Print ζ, Gibson ELIZA

WPI; 1999-243890/20 P-PSDB; AAY05532.

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.

Disclosure; Page 36; 52pp; English

The present sequence is described as a derivative of the human bol-w gene (see AAX25132) and encodes Bol-w protein (see AAY05532), a pro-survival CC member of the Bol-2 family which is widely expressed and which is ce essential for spermatogenesis. The invention relates generally to a CC method of treatment and to an animal model for the identification of CC molecules and genetic sequences useful for inducing or reducing fertility, CC of male animals. Methods are provided for the treatment of infertility, CC or for reducing fertility, by modulating spermatogenesis. An animal model CC carries a mutation is at least one allele of the human or murine bol-w CC gene or in a gene associated with bol-w. Such animals have disorganised CC major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis capable of which can induce infertility

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Best Local Similarity

Matches 531; Conserv
                                                                                                                                      Homo sapiens
                                                                                                                                                                                     Human bcl-y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
 11-FEB-1997;
                       04-AUG-1998
                                             US5789201-A
                                                                                                                                                                                                             02-OCT-1998
                                                                                                                                                                                                                                  AAV28334;
                                                                                                                                                                                                                                                         AAV28334 standard;
                                                                                                                                                            bcl-y; bcl-2;
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 97US-00798897
                                                                   /*tag= a
/product= "bcl-y"
/note= "No stop c
                                                                                                                Location/Qualifiers
                                                                                                                                                              cell
                                                                                                                                                                                                                                                         cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.2%;
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                                                                                                                                                             death
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Pred. No. 3.4e-126;
0; Mismatches 50;
                                                                                                                                                             pathway; apoptotic; apoptosis; human
                                                                                                                                                                                                                                                         ВP
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                                                                     given"
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The mammalian bol-y genes encode a protein that is a member of the bol-2 family, components in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity. Bol-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired
                                                                                                                                                                                Claim 3; Column 15/16; 27pp; English
                                                                                                                                                                                                                  cancers.
                                                                                                                                                                                                                              Nucleic acids encoding B-cell lymphoma-y recombinant protein for use in treating v
                                                                                                                                                                                                                                                                                 WPI; 1998-446079/38.
P-PSDB; AAW61392.
                                                                                                                                                                                                                                                                                                                                   Guastella
                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                   COCENSYS
                                                                                                                                                                                                                                                                                                                                                                                                    96US-0012201P
                                                                                                                                                                                                                                   / protein - useful
uncontrolled cell
                                                                                                                                                                                                                               for producing growth e.g.
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Sequence 579

BP; 106 A; 154

C;

208

G; 111

T; 0 U; 0 Other;

Ś 밁 Ş B δ 片 Ś 밁 δ 맑 Š 밁 δ 片 Ś 멼 δ 밁 S Matches Query Match local 541 541 481 481 421 421 361 361 301 301 181 181 121 241 121 528; 241 61 5 Similarity GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGCCCTGGAGGACGCACGG CAAGTCCACGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATTCCACAGC GTCTTTGGGGCCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGAG CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCCGTCTTGTGGCATTCTTT TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGC ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG AGTGGGGGCTGGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCGTGGCACTG CAGGICTCCGATGAACTTTTTCAAGGGGGGCCCCAACTGGGGGCCGCCTTGTAGCCTTCTTT CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC ATGGCGACCCCAGCCTCGGCCCCAGACACACGCGCTCTGGTGGAAGACTTTGTAGGTTAT Conservative 85.6%; 91.2%; 0; Score 497.4; 1 Pred. No. 3.2e 0; Mismatches 1; DB 2; 3.2e-125; hes 51; 579 579 Indels Length 0; Gaps 540 480 360 360 300 300 240 240 180 180 120 120 60 60 540 480 420 420 0

Job time : 363.378 secs

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Result
No.
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Maximum
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                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
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length: 2000000000
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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US-08-365-486A-14
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US-09-233-527-7
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US-09-010-147B-23

US-09-149-476-130

US-08-081-448-5

US-08-470-670A-6

US-08-481-739-1

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Matches 555
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GENERAL INFORMATION:
                                                                                                                                                                                    TYPE: nucleic STRANDEDNESS: TOPOLOGY: bot
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ALIGNMENTS

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ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2640
INFORMATION FOR SEQ. ID NO: 1:
INFORMATION FOR SEQ. ID NO: 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM For Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                     ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT
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Sequence 1, Application US
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella,
TITLE OF INVENTION: GITTLE OF INVENTION: H
NUMBER OF SEQUENCES:
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ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
THING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ESHOON, 424
ATTORNEY/AGENT INFORMATION:
NAME: ESHOON, 426

PRIOR APPLICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ESHOON, 426

NA
                                 TELEFAX: 202-371-2 INFORMATION FOR SEQ ID
                                                  REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
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; STRANDENNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-08-978-523-1
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US-08-798-897-2
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COUNTRY: USA
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PC-DOS/MS-DOS
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Best Local Similarity
Matches 555; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08798897 Patent No. 5789201
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Guastella,
TITLE OF INVENTION: G
TITLE OF INVENTION: H
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LENGTH: 579 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
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Pred. No. 2.1e-144;
0; Mismatches 24;
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480 480 420 300

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-25400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-798-897-2
                                                                                                                        RESULT 4
US-08-978-523-2
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Sequence 2, Application US/089
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes
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Best Local Similarity
Matches 528; Conserv
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
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Coding For Bcl-y,
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Pred. No. 4e-132;
0; Mismatches 51;
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2640
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.6%;
Best Local Similarity 91.2%;
Matches 528; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 New York Avenue, N.W., Suite 6: CITY: Washington STATE: DC COUNTRY: Washington STATE: DC COUNTRY: USA ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US/08/978,523
FILING DATE: HORDWITCH.
APPLICATION NUMBER: US/08/978,523
FILING DATE: HORDWITCH.
APPLICATION NUMBER: US/08/978,523
FILING DATE: FEBRUARY 11, 1997
CLASSIFICATION 1424
PRIOR APPLICATION 1424
PRIOR 
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LENGTH: 579 base pairs
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: bot
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                                         AGTGGCGGCTGGGGGACTTCACAGCTCTATACGGGGACGGCGCCCTGGAGGACGCACGG
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                                                                                          GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
                                                                                                                                                                                                                                                                                  CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
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Pred. No. 4e-132;
0; Mismatches 51;
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360 360 300 300 240

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LOCATION: 1.1095
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-010-1478-23
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US-09-010-147B-23
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 390; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ni et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/010,147B
FILING DATE: 12-No. 6653445-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MEDIUM TYPE: Flopp:
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
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COUNTRY: U
CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
                                                                                AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGAC 120
                                                                                                                                          ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
                                                                                                                                                                                      ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
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                                              AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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REGISTRATION NUMBER: 41,119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09010147B
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                    Score 364.8; DB 4
Pred. No. 2.6e-94;
0; Mismatches 42
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                                                                                                                                                                                                                                                                              DB 4;
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                                                               EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: 186
FILE REFERENCE: PZ002P1
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
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                                                       APPLIANTE: 1997-05 -27
APPLICATION NUMBER: 60/0
APPLICATION NUMBER: 60/0
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                                              APPLICATION NUMBER:
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                                         60/047,581
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	APPLICATION NUMBER: 60/043, FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043, FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/046, FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056, FILING DATE: 1997-08-22	EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,314 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,311 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,671 EARLIER APPLICATION NUMBER: 60/043,674 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,312 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,312	EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,500 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,598 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,613 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,582 EARLIER APPLICATION NUMBER: 60/047,582 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,596 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,612 EARLIER APPLICATION NUMBER: 60/047,612 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,632 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,632 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER RELIEM DATE: 1997-05-23 EARLIER RELIEM DATE: 1997-05-23 EARLIER RELIEM DATE: 1997-05-23 EARLIER RELIEM DATE: 1997-05-23
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056, R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/048, R FILING DATE: 1997-06-06 R APPLICATION NUMBER: 60/057, R FILING DATE: 1997-09-05 R APPLICATION NUMBER: 60/057, R FILING DATE: 1997-09-05 R APPLICATION NUMBER: 60/056, R APPLICATION NUMBER: 60/056,	FILING DATE: APPLICATION N	1997-05-23 UMBER: 60/047, 1997-05-23	APPLICATION NUMBER: 60/056,8 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,8 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,9 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,8 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,6 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,8

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RESULT 7
US-08-081-448-5
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                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION: NAME: No. 5646008thrup,
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
                                           APPLICATION NUMBER: US
FILING DATE: 19930622
                              FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                   STREET:
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ER APPLICATION NUMBER: 60/057,669
ER FILING DATE: 1997-09-05
ER PILING DATE: 1997-06-13
ER FILING DATE: 1997-06-13
ER APPLICATION NUMBER: 60/061,060
ER FILING DATE: 1997-10-02
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No. 5646008thrup,
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5646008th Clark Street, Suite 800
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                                                            US/08/081,448
 Thomas
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Pred. No. 4.1e-94;
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                                                                                            Version
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US-08-470-670A-6
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Best Local Similarity
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
APPLICANT: BOISE, Lawrence H.
TITLE OF INVENTION: COMPOSITIONS AND METH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FEATURE:
                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White
STREET: P.O. Box 4433
                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                              STREET:
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TOPOLOGY: lir
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                ZIP:
                                                                                              COUNTRY:
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REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEPAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG
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AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG
                                            GGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCG
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58.3%;
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RESULT 9
US-08-481-739-1
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                                                                                                                         Sequence 1, Application US/08481739
Patent No. 6143291
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081
FILING DATE: 22-UU-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
LOCATION:
                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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                                                       STREET:
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TYPE: nucleic acid
STRANDEDNESS: single
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Massachusetts
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                                                      28 State Street
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Pred. No. 7.1e-29;
0; Mismatches 169;
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Best Local Similarity
Matches 236; Conserv
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APPLICATION NUMBER: US 08/-
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RP.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUNE-1
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OPERATING SYSTEM:
SOFTWARE: PatentI
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AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG
                                                                                                   GCTGGGCGGACTTCACAGCTCTATACGGGGACGGGCCCTGGAGGACGCACGGCGTCTGC
                                                                                                                                     CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG
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                                                                 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC
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SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/09167921A
Patent No. 6172216
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.

RESULT 10 US-09-167-921-1

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US-09-277-020-39
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                                                                                                        Sequence 39, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
FILE REFERENCE: ISPH-0339
CURRENT FILING DATE: 1999-03-67,020
CURRENT FILING DATE: 1999-03-67,921
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
NUMBER: 05 SEQ ID NOS: 65
NUMBER: 05 SEQ ID NOS: 65
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Best Local Similarity
Matches 236; Conserv
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SEQ ID NO 1
LENGTH: 926
                                                                               SOFTWARE: PatentIn
SEQ ID NO 39
TYPE: DNA
ORGANISM: Homo :
-09-277-020-39
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
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CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
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ORGANISM: Homo :
FEATURE:
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TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
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                                                                LENGTH: 926
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                                                                                                   Ver.
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APPLICANT: Bennett, C. Frank
APPLICANT: Mennett, C. Frank
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (115)..(836)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1994-07-26
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                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6214986 GENERAL INFORMATION:
                                                                                   Query Match
Best Local
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Best Local Similarity
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AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG
                               ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCCACCTTCTCTG
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Pred. No. 7.1e
0; Mismatches
                                                                  Score 134.6; DB 3;
Pred. No. 7.1e-29;
0; Mismatches 169;
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US-08-461-511A-6
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US-08-461-511A-6
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Query Match
Best Local Similarity
Matches 236; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-0un-1995
CLASSIFICATION: UNKNOWN
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARCD:179

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEPAX: (512) 474-7577
                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       754
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                                                                                                                                                                          LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGGGCGGACTTCACAGCTCTATACGGGGACGGCCCTGGAGGACGCACGGCGTCTGC
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COUNTRY: United States of
                                                                                                                            NAME/KEY:
                                                                                                                                                           TOPOLOGY: linear
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   Conservative
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135..836
                  23.2%;
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   0
 Score 134.6; DB 4;
Pred. No. 7.1e-29;
0; Mismatches 169;
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US-09-271-014A-5
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 926
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
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Local Similarity 58.3%;
les 236; Conservation
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                                                                                                                                           CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGCATTCTTTGTCTTTG
                                                                                                                                                                                                                PatentIn Ver.
AGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCG
                                  GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG
                                                                     GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTCC
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634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG
AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG
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Sequence 5, Application US/09271014A Patent No. 6395510 FILE REFERENCE: ARCD:316
CURRENT APPLICATION NUMBER: US/09/271,014A
CURRENT FILING DATE: 1999-03-17 APPLICANT: THOMPSON, CRAIG B.
APPLICANT: BOISE, LAWRENCE H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS Score 134.6; DB 4; Pred. No. 7.1e-29; 0; Mismatches 169;

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Indels Length 926;

0

Gaps

453 187

367 573 307 513 247

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US-09-023-655-1430
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                                                                                                                                         Query Match
Best Local Sim
Matches 236;
                                                                                                                                                                                                                                                                                                                  TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPB: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
COMPUTER: PC DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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APPLICATION NUMBER:
FILING DATE:
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STREET: 9ALO ALTO
CITY: PALO ALTO
CTATE: CALIFORNIA
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ADDRESSEE: INCYTE PHARMACEUTICALS,
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                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                         ACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCCAGGTTT 247
                                                                    AGCAAGCGCTGAGGGAGGCAGGCGACGACTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                                                                    ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTG 187
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Pred. No. 7.1e-29;
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 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG
                                 GGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCG 532
                                                                 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC
                                                                                                                                                                       AGGATTGGATCGTGGCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGCAGTGGCG 427
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Search completed: March 29, 2004, 07:30:35 Job time : 78.3686 secs

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Minimum DB seq length: 0
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Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_manmal:*
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9: sp_bhage:*
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Gapop 10.0 , Gapext 0.5
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SUMMARIES
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Result No.	Score	Query Match	Length	BB	ID	Description
1	1005	99.6	193	11	088996	O88996 rattus norv
2	1005	99.6	219	11	Q7TS60	Q7ts60 rattus norv
ω	965	95.6	193	11	Q8CGL4	
4	770	76.3	178	11	Q9CYW5	Ψ.
υ	770	76.3	178	11	QBCFR2	
6	439.5	43.6	233	თ	Q9MYW4	oryc
7	435.5	43.2	233	11	035844	O35844 mus musculu
00	432.5	42.9	233	σ	Q8SQ42	Q8sq42 felis silve
9	431.5	42.8	233	σ	Q9N1A2	Q9nla2 sus scrofa
10	428.5	42.5	233	თ	Q9MZS7	Q9mzs7 ovis aries
11	412	40.8	236	11	Q8BQK4	Q8bqk4 mus musculu
12	412	40.8	236	1	Q7TSN8	Q7tsn8 rattus norv
13	406	40.2	79	11	Q7TS61	Q7ts61 rattus norv
14	401	39.7	180	თ	Q9BDD5	Q9bdd5 bos taurus
15	401	39.7	217	片	Q99N35	Q99n35 mus musculu
16	400	39.6	238	13	Q90Z98	Q90z98 brachydanio

4. U	44	43	42	41	40	39	3 B	37	36	ω UI	ω 4	ω U	3 2	31	30				8								18	17	
148.5	149	151	154	154	156.5	157.5	162	163	168.5	170.5	172.5	174.5	182	185	187	296	342.5	347	353	365.5	371	77	374.5	7,4	8	95	398	398.5	
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Q9N754	08SQ43	Q8MJB3	Q9JKL3	Q8WZ49	Q8K3J2	Q9MZS6	Q9R1B3	Q967D2	Q9H1R5	Q8NFF3	Q98U13	Q9I9N4	Q8C264	Q9WUI5	Q9JK59	Q8UWJ1	Q8C5P0	Q99N36	Q8MJB1	Q7YRB6	Q90ZH2	Q9H1R6	035843	Q9QWX2	Q7TS62	Q8I008	Q923R6	Q9BDX7	
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ALIGNMENTS

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Fiam; PF02180; BH4; 1.	Pro; IPR002475; BCL2	InterPro; IPR003093; Bc12_BH4.	06915; P:apoptosis;	GO:0016329; F:apoptosis r	Q07817; 1MAZ.	EMBL; AY185098; AA064468.1;	EMBL; AF096291; AAC64200.1;	J. Neurochem. 85:1500-1512(2003).	BCT-2-retaired protein ramity gene expression during origodendrogriat	sure D.,	ed=1	STRAIN=Sprague-Dawley;	SEQUENCE FROM N.A.		ce 91:673-684(1999).	d adult rat nervous system.";	ial expression	Hamner S., Skoglosa Y., Lindholm D.;	MEDLINE=99292146; PubMed=10366024;	STRAIN=Sprague-Dawley; TISSUE=Brain;	SEQUENCE FROM N.A.			a; Sciuroqnathi; Muridae; Murinae	Chordata.	100000000000000000000000000000000000000	BCI-w.	(TrEMBLrel. 25, Last annotation	(TrEMBLrel. 08, Last	-1998 (TrEMBLrel. 08,	88996;	O88996 PRELIMINARY; PRT; 193 AA.	ILT 1 996

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Best Local Sim
Matches 192;
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Best Local Sim
Matches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM0033/; SC., SMART; SM00265; BH4; 1.

PROSITE; PS00022; BCL2 FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01280; BH2; 1.

R PROSITE; PS01260; BH4_1; 1.

R PROSITE; PS01260; BH4_1; 1.

R PROSITE; PS01260; BH4_2; 1.

R PROSITE; PS0003; BH4_2; 1.

R PROSITE; PS0003; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Q7TS60;
Q7TS60;
01-0CT-2003
01-0CT-2003
01-0CT-2003
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE=22672518; PubMed=12787069;
Itoh T., Itoh A., Pleasure D.;
                                                                                                                                                                                                                                                                                                                                                                                                            BCL-WEL.
                                                                                                                                                                                                                                        "Bcl-2-related protein family gene differentiation.";
J. Neurochem. 85:1500-1512(2003).
EMBL; AY185100; AA064470.1;
SEQUENCE 219 AA; 23720 MW; 30E3
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                     Similarity
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                     GALVTVGAFFASK 193
                                                            QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                           MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                          MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                             FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                            FSDLAAQLHVTPGSAQQRFTQVSDELFQGGBNWGRLVAFFVFGAALCAESVNKEMEPLVG
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                                               QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                        23720 MW; 30E36041BC1DC66F CRC64;
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                                                                                                                                                                                                      99.6%;
219
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                                                                                                                                                                                         Score 1005; DI
Pred. No. 4.6e:
0; Mismatches
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Last sequence update)
Last annotation updat
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Pred. No. 3.
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                   DB 11;
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Mus musculus (Mouse).
Eukaryota; Metazoa; C.
Mammalia; Eutheria; R.
NCBI—TaxID=10090;

Chordata; Rodentia;

Craniata; Veri Sciurognathi;

Vertebrata; Euteleostomi; thi; Muridae; Murinae; Mus

BCL2L2

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

17, 17, 24,

Created)

Last sequence update)
Last annotation updat

update)

[1]
SEQUENCE FROM N.A.
TISSUE-Embryo:

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RESCRIPTION OF STREET OF S
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Best Local
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Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                     Q9CYW5;
01-JUN-2001 (
01-JUN-2001 (
01-JUN-2003 (
Bc12-like 2.
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Q8CGL4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9CYW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2002) to the EMEL; AY170344; AA013177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bcl2-like protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Su H.-Y
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Rodentia;
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Pred. No. 1.4e-77;
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RESULT.

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Best Local Sim
Matches 145;
                                                                                                                                                                                          Q8CFR2;
Q8CFR2;
01-MAR-2003
01-MAR-2003
01-OCT-2003
Bc12-like 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

PROSITE; PS01080; BCL2; FAMILY; 1.

PROSITE; PS01080; BH4; 1.

PROSITE; PS01260; BH4 1; 1.

PROSITE; PS0063; BH4 2; 1.
                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:108652; Bcl2l2.
GO; GO:0016339; Frapoptosis regulator activity;
GO; GO:006515; Frapoptosis; IEA.
InterPro; IPR000712; Bcl2_BH.
InterPro; IPR003093; Bcl2_BH4.
InterPro; IPR003093; Bcl2_Family.
Pfam; PF00452; Bcl2_; 1.
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Nature 409:685-690(2001).
EMBL; AK013244; BAB28740.1; -.
SEQUENCE FROM N.A.
TISSUE=Eye;
Strausberg R.;
                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q07817;
                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDBFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                              QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQDWMVAYLETRLADWIHSSGGWAEFTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSDLAAQLHVTPGSAQQRFTQVSDELFQGGFNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1MAZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.3%;
96.7%;
                                                                                                                                                                                                                  223,
                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 770; DB 11;
Pred. No. 2.3e-60;
1; Mismatches 4
                                                                                                           Craniata; Vertebrata; Euteleostomi
Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E2D4C3F79528E9D7 CRC64;
                                                                                                                                                                                                                                                                                                     178
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                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
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Best Local S
Matches 145
         InterPro; IPR003093; Bc12_BH4.
InterPro; IPR003475; Bc12_family.
InterPro; IPR004725; Bc12_reg.
Pfam; PF00452; Bc12_reg.
Pfam; PF00452; Bc12_1 1.
SMART; SM00337; Bc1; 1.
SMAXT; SM00337; Bc1; 1.
SMAXT; SM00365; BH4; 1.
FROSITE; PS00062; BC12_FAMILY; 1.
PROSITE; PS01060; BH3; 1.
PROSITE; PS01060; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH44_2; 1.
PROSITE; PS01260; BH44_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000
01-OCT-2000
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00265; BH4; 1.

PROSITE; PS01080; BC12 FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01260; BH4 1; 1.

PROSITE; PS50063; BH4 2; 1.

SEQUENCE 178 AA; 19119 MW; E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00337; BCL;
SMART; SM00265; BH4;
                                                                                                                                                                                             GG; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR000712; Bc12_BH.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9MYW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9MYW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016329; F:apoptosis regulator GO; GO:0006915; P:apoptosis; IEA. INTERPROPOSIS; BELZ BH. INTERPRO; IPRO03093; BELZ BH4. INTERPRO; IPRO03475; BELZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC040369; AAH40369.1; MGD; MGI:108052; Bc1212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                  EMBL; AY005131; AAF88137.1;
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                        "Rabbit Bcl-X.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQDWMVAYLETRLADWIHSSGGWAEFTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATPASTPOTRAL VADFVGYKLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                   cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                      Robertson L., James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%;
96.7%;
 25986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
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Pred. No. 2.3e-60;
 12F0F30344D53F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E2C3F3F79528E9D7 CRC64;
                                                                                                                                                                                                                                                                                                      E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity; IEA
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                                                                                                                                                                                                                           IEA
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                                                                Query Match
Best Local S
Matches 94
                                                                                                                                                                                        ANNULLLLY ':027039119'.'

REMEL' US1278; AACS3459.1; -.

HSSP; P53563; 1AF3.

MGD; MGI:88133; BC121.

GG; GG:001016020; C:membrane; IEA.

GG; GG:0016329; F:apoptosis; regulator activity; IE;

GG; GC:0016329; F:apoptosis; IEA.

InterPro; IPR000712; BC12_BH4.

InterPro; IPR003093; BC12_BH4.

InterPro; IPR003093; BC12_FAmily.

InterPro; IPR004775; BC12_Family.

InterPro; IPR004775; BC12_reg.

Pfam; PF00452; BC1-2; 1.

SMART; SM00337; BC1-1;

PROSITE; PS01080; BH4; 1.

PROSITE; PS01180; BH4; 1.

PROSITE; PS01180; BH1; 1.

PROSITE; PS01180; BH1; 1.

PROSITE; PS01180; BH1; 1.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            035844;
01-JAN-1998
01-JAN-1998
01-JUN-2003
                                                                                                                                PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H.; "A novel Bel-x isoform connected to apoptosis in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                035844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mmunity 7:629-639(1997).
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                                1
                                                              94;
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   σ
                                                                                                                                                                                 PS50062; BCL2 FAMILY; 1
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01258; BH2; 1.
                                                                                                                             ; PS01259; BH3; 1.
; PS01260; BH4_1; 1.
; PS50063; BH4_2; 1.
E 233 AA; 26033 MW
                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV
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                                 RALVADFVGYKLROKGY-----
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 RELVVDFLSYKLSOKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.) (TrEMBLrel.)
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                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Thymus
                                                                                 43.2%;
                                                                                                                                26033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 439.5;
; Pred. No. 5.9e
22; Mismatches
                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                 Score 435.5;
Pred. No. 1.3
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                                                                                                                                3083F2D8327E072E CRC64;
                                                                 Mismatches
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                                                                                 .3e-30;
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                                                                                                DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
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01-JUN-2002 (TrE
01-JUN-2003 (TrE
BC1-x1 protein.
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                  NGGWDTFVELYGNNAAAESRK--
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PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS05063; BH4 1; 1.
PROSITE; PS50063; BH4 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00452; BC1-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
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"Moleculer cloning of feline Bcl-2 family.";
submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AB080951; BAB85856.2;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator activity
GO; GO:0006915; P:apoptosis; IEA.
TITESCATA: TITESC
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Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR000712; Bc12_BH.
InterPro, IPR003093; Bc12_BH4.
InterPro, IPR002475; BC12_Edmily.
InterPro, IPR004725; Bc12_reg.
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                                                                        SGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                  NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
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Pred. No. 2.5e-30;
3; Mismatches 58
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; Fissipedia; Felidae;
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Best Local S
Matches 94
                                                                                            Q9MZS7;
01-OCT-2000
01-OCT-2000
01-JUN-2003
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Q9N1A2;
01-OCT-2000
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01-OCT-2000 (TrEMBLrel. 1
01-JUN-2003 (TrEMBLrel. 2
Anti-apoptotic regulator
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SMART; SM00265; BH4;
TIGRFAMS; TIGR00865;
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InterPro; IPR00303; Bc12_BH4.
InterPro; IPR003475; Bc12_family.
InterPro; IPR004725; Bc12_reg.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
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GC; GC:0016020; C:membrane; IEA.
GC; GC:0016329; F:apoptosis regulator
GC; GC:0016329; P:apoptosis; IEA.
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"PCR Cloning of a Porcine bcl-:
Submitted (DEC-1999) to the EM
EMBL; AF216205; AAF33212.1; -.
                                                                                                                                                                                                                      Q9MZS7
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Mammalia; Eutheria;
   Eukaryota;
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E; PS50062; BCL2 FAMILY; 1.

E; PS01080; BH; 1.

3; PS01258; BH2; 1.

3; PS01258; BH3; 1.

3; PS01260; BH4 1; 1.

3; PS01260; BH4 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEFWIQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RALVADFVGYKLRQKGY------
                                (Sheep).
                                                                                   ) (TrEMBLrel.
) (TrEMBLrel.
3 (TrEMBLrel.
   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26047 MW;
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. 15, Last
. 24, Last
or Bcl~xL.
                                                                                            15,
15,
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Last ann
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EMBL/GenBank/DDBJ datab
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   Craniata;
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2FA312818B25E17D CRC64;
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                                                                                            sequence up
annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity;
   Vertebrata;
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                                                                                         update)
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   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                          183
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RESULT 11
Q8BQK4
   RRRRRRR ROCCOS GREAT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO0865; bc1-2; 1.
PROSITE; PS50062; BC12 FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4-1; 1.
PROSITE; PS01260; BH4-2; 1.
PROSITE; PS05063; BH4-2; 1.
SEQUENCE 233 AA; 26134 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00452; BC1-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                  Q8BQK4;
01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Caprinae, Ovis.
NCBI_TaxID=9940;
                                                                                                                                             BCL2.
MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium, the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murray J.F., Dong Y.B., Leigh A.J., "BGL-x in the sheep ovary."; Submitted (UTL-199) to the EMBL/GeEMBL; AF164517; AAF89532.1; -.
                                                                       SEQUENCE FROM N.A.
                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                        B-cell leukemia/lymphoma
                                                                                                                                                                                                                   Q8BQK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                            STRAIN=C57BL/6J;
                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002475; InterPro; IPR004725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000712;
InterPro; IPR003093;
                                                                                                                                                                                                                                                                                                    142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                          NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               RALVADFVGYKLROKGY-----
                                                                                                                                                                                                                                                                                                                                         VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS
                                                                                                                                                                                                                                                                                                                                                                                                D------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                       RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                   GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                                                           VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN
                                                                                                                                                                                                                                                                            GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                  PRELIMINARY;
                                                         TISSUE=Body;
                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC12_BH.
BC12_BH4.
BC12_family.
BC12_reg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 428.5; DB (
Pred. No. 5.6e-30,
                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     012BFA1382762915 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                            Mus
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annotation Team;

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В
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Q7TSN8
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Best Local S
Matches 87
                                                                              Best Loc
Matches
                                                                                                                 Query Match
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Q7TSN8;
Q7TSN8;
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PF00452; BC1-2; 1.—
PEAM; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
TIGREAMS; TIGR00865; bC1-2; 1.
PROSITE; PS0062; BC12_FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005829; C:cytosol; IDA.
GO; GO:00058189; F:apoptosis inhibitor ac
GO; GO:0005815; F:protein binding; IPI.
GO; GO:0005915; P:apoptosis; IDA.
InterPro; IPR000712; Bcl2_BH.
InterPro; IPR003093; Bcl2_BH.
InterPro; IPR002475; Bcl2_Family.
InterPro; IPR004775; Bcl2_reg.
Pfam: PR00475; Bcl2_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                   Tanaka T., Nangaku M.;
"Rat Bc12-11ke protein.";
"Rat Bc12-11ke protein.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF512835; AAA47159.1; -.
SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;
                                                                                                                                                                                                                                             SEQUENCE FROM I
STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                            Bcl2-like protein.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                 Local
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AK049473; BAC33767.1;
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                                                                              87; Conserv
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PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                          DTRALVADFVGYKLRQKGYVCGAG-----
                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLRPLVATTGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNREIVMKYIHYKLSORGYEWDÄGDADAAPLGAAPTPGIFSFOPESNPMPAVHRDMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTRALVADFVGYKLRQKGYVCGAG------PG------
       DNREI VMKY I HYKLSQRGYEWDAGDADAAPLGAAPTPGI FSFQPESNPMPAVHRDMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA;
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                               40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.8%;
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                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 412; DB
Pred. No. 1.6e-
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                            Score 412; DB 11;
Pred. No. 1.6e-28;
4; Mismatches 59;
                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B726BFFA3AA1C718
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                                              ----PG---
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Query Match
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01-OCT-2003
01-OCT-2003
SEQUENCE FROM N.A.
Amills M., Bouzat J.;
Amills M., Bouzat J.;
"Characterization of the bovine bc1-xL gene and rela
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databa
SMBL; AF245488; AAK31307.1; -.
EMBL; AF245489; AAK31308.1; -.
HSSP; Q07817; 1MAZ
GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                          O9BDD5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Anti-apoptotic regulator Bcl-xL (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE=22672518; PubMed=12787069;
Itoh T., Itoh A., Pleasure D.;
                                                                                                                                                                                                                                                               Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                       Q9BDD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation.";
J. Neurochem. 85:1500-1512(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Bcl-2-related protein
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCL-WS.
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nilarity 98.7%;
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Rodentia;
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SO PRO DR

InterPro; IPR000712; Bcl2_BH.
InterPro; IPR002475; BcL2_family.
Pfam; PF00452; Bcl-2; 1.
SMART; SM00337; BcL; 1.
PROSITE; PS50062; BcL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.

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InterPro; IPR002475; Bcl2_family.
InterPro; IPR002475; Bcl2_reg.
Pfam; PF00475; Bcl-2; 1.
SMART; SM00337; Bcl; 1.
ITGRFAMG; TTGR00865; bcl-2; 1.
PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang X.-F., Cantor H.;
"Novel cDNA structure and genomic organization of apoptosis regulatory gene Bcl-x-gamma.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133282; AAK15455.1; -.
EMBL; AF133281; AAK15455.1; JOINED.
HSSP; P53563; 1AF3.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
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GO:0016329; F:apoptosis regulator activity; IEA.
GO:0006915; P:apoptosis; IEA.
QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG
                                                                                                                                                                                                                       217 AA;
                                                                           Conservative
                                                                                                                                                                                                                           24234 MW;
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53.5%;
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                                                                       Score 401; DB 11; Length Pred. No. 1.4e-27; 9; Mismatches 45; Indels
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                                                                       Indels
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RESULT 15 Q99N35

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104 AALCAESVNKEMEPLYGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163

GALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ 157

44 QAMRAAGDEFETRFRRTFSDLAAQLEVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103

QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG

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39.7%; Score 401; DB 6; Length 18 ilarity 53.5%; Pred. No. 1.1e-27; Conservative 19; Mismatches 45; Indels

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PS01259; BH3; 1.

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158 164

ERFNRWFLTGMTVAGVVLLGSL 179 E--GNWASVRTVLTGAVALGAL 183

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                       164 E--GNWASVRTVLTGAVALGAL 183
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ALIGNMENTS	A32758	GNWVWV	H95160	G98026	AJICQB	B97381	AI2598	T36534	GNWVKV	B83217	I49449	A47476	I39055	JC7567	138921	S54778	
	beta-amyloid-like	genome polyprotein	alanyl-tRNA synthe	alanine-tRNA ligas	glutamate-ammonia	dihydrodipicolinat	dihydrodipicolinat	probable lipase/es	genome polyprotein	hypothetical prote	hemopoietic-specif	BCL2 homolog MCL1	Bcl-2 related - hu	Mcl-la protein - z	bcl-2-associated p	NR-13 protein - qu	

bcl-x long - mouse bcl-x long - mouse bcl-x long - mouse Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: nuscolus equence_revision 02-Jul-1996 #text_change 28-Jul-2003 C;Accession: I49056; S52866 R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W. J. Immunol. 153, 4388-4398, 1994 A;Title: Cloning and molecular characterization of mouse bcl-x in B and T l A;Reference number: 149055; MUID:95052604; PMID:7963517 A;Accession: I49056 A;Accession: I49056 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-233 <KAM> A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623 C;Superfamily: bcl apoptosis regulator, inhibitory type A,Cross-references: EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g506648 R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M. submitted to the EMBL Data Library, November 1994 A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B coaperage of the property of the p 밁 S В 8 밁 Ş 밁 5 A; Accession: S52866 A; Molecule type: mRNA A; Residues: 1-233 < RES > Matches Query Match Local 141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183 125 81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNXEMEPLVGQVQDWWVAYLETRLADWIHS 140 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 11 RAIVADFVGYKLRQKGY-----V 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 93, σ Similarity RELVVDFLSYKLSOKGYSWSOFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE Conservative 41.3%; 42.5%; 22; Mismatches Score 428.5; DB 2 Pred. No. 2.2e-32; DB 2; Length 233; 57; Indels 53; Gaps T lymphocytes 80 65 28 124 4 line

apoptosis regulator bcl-xL - human N;Alternate names: bcl-2-related protein N;Contains: apoptosis regulator bcl-xS

RESULT B47537

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R;Boise, L.H.; Gonzalez-Garcia, M.; rublema, C.D., 2007-608, 193
Cell 74, 597-608, 193
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of A;Reference number: A47537; MUID:93364977; PMID:8358789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:BCL2L
A;Gene: GDB:BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status pre-
F;1-125,189-233/Product: apoptosis regulator bcl-xS #st
                                                                                  A; Molecule type: DNA
A; Residues: 1-125,189-233 <MI2>
A; Cross-references: EMBL: X82537; NID: g607176;
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A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references:
A;Accession: C47537
                                                                                                                                                                A;Experimental source: embryonic; A;Accession: S51762
                                                                                                                                                                                     A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177
A;Experimental source: embryonic; brain
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-233 < MIC>
                                                                                                                                                                                                                                                                              A; Reference number: S51761
A; Accession: S51761
                                                                                                                                                                                                                                                                                                                    R;Michaelidis, T.M. submitted to the EMBL Data
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                                                    A; Note: smaller form due to splicing
                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                     ;Species: Rattus norvegicus
;Date: 07-May-1995 #sequence
;Accession: S51761; S51762
                                                                       Experimental source:
Superfamily:
                   Introns: 125/3
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apoptosis regulator,
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                                                                         embryonic;
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_revision 01-Sep-1995 #text_change 28-Jul-2003
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Pred. No. 2.8e
23; Mismatches
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inhibitory
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les 59;
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type
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#status predicted
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Query Match

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Score

424.

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DB 2;

Length

A;Status:

preliminary

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transforming protein (bcl-2-alpha) - chicken
(;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
C;Accession: A37332; S35453
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 192
A;Title: Isolation and characterization of the chicken bcl-2 gen
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Reference number: A37332 MUID:92375724; PMID:1508712
A;Accession: A37332
A;Status: nucleic acid sequence not shown
A,Molecule type: DNA
A,Residues: 1-233 < EUIT.
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C. Biochim. Biophys. Acta 1132, 109-113, 1992
A;Title: Molecular cloning and DNA sequence analysis of cDNA A;Reference number: S24390; MUID:92379084; PMID:1511008
A;Accession: $24390
                                                                                                       transforming protein (Bc1-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S24390
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C; Superfamily: b
C; Keywords: mito
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: bcl apoptosis regulator, Keywords: mitochondrion; transforming
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Pred. No. 6.5e
32; Mismatches
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2; Mismatches 56;
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transforming protein bcl-2, splice form alpha - human (;Species: Homo sapiens (man) (;Cpate: 31-Dec-1988 #sequence revision 07-Jun-1996 #text_change 28-Jul-2003 C;Accession: C37332; A29409; S02452; A24428; A27622; B27622 R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression; C37332; MUID:92375724; pMID:1508712 A;Accession: C37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-232 <CAZ-A,
A;Cross-references: EMBL:Z11961; NID:962969; PIDN:CAA78018.1;
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: mitochondrion; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: this report is a correction R;Tsujimoto, Y.; Croce, C.M.
R;Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, and protein A;Reference number: A29409; MUID:86259760; PMID:3523487
                                                                 A;Residues: 1-58,'T',60-116,'R',118-239 <CLB>
A;Cross-references: GB:M14745; NID:g179370; PID:AAA35591.1; PID
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wri
Oncogene Res. 2, 263-275, 1988
A;Title: Consequences of the t(14;18) chromosomal translocation
A;Reference number: A27622; MUID:88217344; PMID:3285301
                                                                                                                                                                                                                                                   A;Title: Cloning and structural analysis of cDNAs for bcl-2
A;Reference number: A24428; MUID:87002488; PMID:2875799
A;Accession: A24428
                                                                                                                                                                                                                                                                                                                            R;Cleary, M.L.; Smith, S.D.;
Cell 47, 19-28, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-95, 'A', '97-109, 'G', 111-236, 'S', 238-239 <TSU's
A;Residues: 1-95, 'A', '97-109, 'G', NID:9179366; PIDN:AAA51813.1; PI
A;Rose-references: GB:M13994; NID:9179366; PIDN:AAA51813.1; PI
A;Note: this sequence has been corrected in reference A37332
A;Note: this sequence has been corrected in reference A37332
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett,
EMBO J. 7, 123-131, 1980
A;Title: Alternative promoters and exons, somatic mutation and
A;Reference number: S02452; MUID:88196071; PMID:2834197
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A; Residues: 1-239 <SET>
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A; Residues: 1-239 < EGU >
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P; P;
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A; Residues: 1-58, 'T',
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                                               Accession: A27622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLVRCPRLRGCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEE 129
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  , 'T',
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37.7%; Pred. No. 4.9e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
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Wright, J.J.;
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,60-239

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190

GGWDAFVELYG----PSMRPLFDFSWQSLKTULSLAL-VGACITLGAYLGHK GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK

142 130

VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN

189

141

VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS

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A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline constitutive expression of BCL2 following to cycenetics:
                                                                                                                                                                                                                                                                                                                  R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid
A;Reference number: 153295; MUID:95129487; PMID:7828536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: blocks apoptosis in hematopoietic cells C;Superfamily: bcl apoptosis regulator, inhibitory type C;Keywords: alternative splicing; apoptosis; B-cell lymphoma;
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                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 26-Jul-1996 #sequence_revision C;Accession: I67432
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C;Species: Rattus norv
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                                                                                                                                                                                                                                                A; Residues: 1-236 < RES>
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A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLQTPAAPGAAAGPALSPVPPVVHLTLKQAGDDFSRRYKRDFAEMSSQLHLTPFTARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNREIVMKYIHYKLSORGYEWDAGDVGAAPPGAAPAPGIFSSOPGHTPHPAASRDPVART
SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                  ----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                       DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART
                                                                                                      DTRALVADFVGYKLRQKGY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI
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                                                                                                                                           Conservative
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                                                                                                                                                          40.7%;
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Pred. No. 8.8e-31;
                                                                                                                                                           Score 411;
Pred. No. 9
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C;Species: Mus muscurus (C)Date: 31-Dec-1988 #sequence
C;Date: 31-Dec-1988 #sequence
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; KC
Cell 49, 455-463, 1987
                                                                             A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109
R;Eguchi, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vai
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tayMolecule type: DNA
A;Residues: 1-33, E, 34-220, AL', 223-236 <EGU>
C;Genetics:
A;Gene: BCL2
A;Introns: 192/3
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
TVMSA1
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C;Superf
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A; Title: Cloning and sequencing of a cDNA encoding the rat
A; Reference number: IS3744; MUID:94193015; PMID:8144041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene bcl-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29
C;Accession: I53744
R;Sato, T.; Irie, S.; Krajewski, S.; Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary; translated A,Molecule type: mRNA A,Residues: 1-236 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: I53744
                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-236 < NEG >
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Best Local S
Matches 83
  Query Match
Best Local S
Matches 86
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    66;
                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVEELFRDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
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    Conservative
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                     40.1%;
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Score 405; DB
Pred. No. 3.5e
33; Mismatches
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Pred. No. 2.8e-30;
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                                            DB 1;
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C;Accession: 167431

R;Tilly, J.I.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 115, 232-241, 1995

A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-Xlong messenger ribonucleic acid A;Reference number: 153295; MUID:95129487; PMID:7828356

A;Accession: 167431
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A;Residues: 1-233 <RES>
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Best Local
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 185
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                                 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                      OVSDELFOGGENNGRLVAFFVFGAALCAESVNKEMEFLVGOVODWMVAYLETRLADWIHS 140
                                                                                                                                                                             CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                       RALVADFVGYKLRQKGY-----
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 NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                    QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                             NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124
                                                                                                                                                                                                                  RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                       40.18;
                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                           Score 404.5;
Pred. No. 3.8
                                                                                                                                                                                                                                                                                                         3.8e-30;
                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            levels.
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                                     183
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B-cell lymphoma 2 protein - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000
C:Accession: JC7383
                                                                                                                                         R;Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903,
A;Title: Cloning and functional analysis of
A;Reference number: JC7383
A;Cross-references: GB:AJ271720
C;Comment: This protein has ant:
C;Genetics:
                                                         A; Molecule type: mRNA
A; Residues: 1-236 < TOM>
                                                                                                  A; Accession: JC7383
                                                                                                                          A; Contents: Ovary
                   has anti-apoptotic
                   function,
                                                                                                                                                                  CDNA
                                                                                                                                                                  encoding
                                                                                                                                                                                                                                               #text_change
                     and
                   supports
                                                                                                                                                                  the
                                                                                                                                                                    hamster
                     cell
                                                                                                                                                                    Bc1-2
                       survival
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protein

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RESULT 12
A47537
AA7537
apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Aate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C;Accession: A47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Accession: A47537
A;Status: preliminary
RESULT 13
149057
149057
bc1-x transmembrane deleted - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C:Accession: I49057
C:Faccession: Nivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bc1-x in B and T 1:A;Reference number: I49055; MUID:95052604; PMID:7963517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-190 <BOI>
A;Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1;
C;Superfamily: bcl apoptosis regulator, inhibitory type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: bcl-2
C;Superfamily: bcl
C;Keywords: B-cell
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Best Local S
Matches 81
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                                                                                                                                                                                                                                                                                                                           LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV
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Pred. No. 8.6e-28;
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RESULT 15 B37332

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A;Gene: bcl-x
A;Map position:
C;Superfamily: b
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A;Residues: 1-214 <RES>
A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl apoptosis regulator, inhibitory type
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A;Status: preliminary; translated
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A; Residues: 1-227 <BAN>
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                                                                                                                          66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                          29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
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NGGWVRTKPLVCPFSLASGQR
                             SGGWAEFTALYGDGALEEARR 161
                                                             QVVNELFRDGVNWGRIVAFFSFGGAL
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                                                                                                                                                                                          RELVVDFLSYKLSOKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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bcl apoptosis regulator,
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Pred. No. 1.1e
16; Mismatches
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C;Accession: B37332; S35452
R;Bguchi, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: B37332
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Residues: 1-216 < EGGU'>
A;Cross-references: EMBL:D11381; EMBL:D11382
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl apoptosis regulator, inhibitory type
Search completed: March 25, 2004, 15:45:07 Job time: 15 secs
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                                                                                                                                                 145 AEFTA 149
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                                                                                                                                                                                                     130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSFLVDNIATWMTEYLNRHLHNWIQDNGGW 189
                                                                                                                                                                                                                                   85 ELFQGGDNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHSSGGW 144
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Minimum DB |
Maximum DB |
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Maximum Match 10
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seq length: 2000000000
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1009
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                                                                                                                                                                                                                                                                                                                                                       1586107 segs, 282547505 residues
                                                                                                                             A_Geneseq_29Jan04:*
1: geneseqp1980s:*
                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATPASTPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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                                                                                             geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	B	ID	Description
	00	0 !	193	νį	AAY05531	Aay05531 Mouse Bcl
N	1005	99.6	193	N	6139	391 Rat bcl-
ω	0	9	193	N	ω	91
4	00	9	192	N	73	93 Protein
ທ	1000	99.	193	N	553	5530
σı	1000	99.	193	7	74	Add46742 Human Pro
7	995	98.	193	N	39	392
0 0	995		193	Ŋ	39	w
9	993	98.	193	N		Aaw36047 Human bcl
10	993	98.	193	N	55	Aay05532 Human Bcl
11	990	98.	192	N	739	Aaw97394 Mammalian
12	967.5	95.	192	N	553	3 Mouse
13	876	86.	168	N	AAW36048	Aaw36048 Mouse bcl
14	814.5		190	ທ	AA018223	3 Human Bc
15	759	75.	365	N	AAW59884	Aaw59884 Amino aci
16	759	75.	365	v	U	
17	759	75.	365	9	ABO34750	Abo34750 Fragment
18		42.	411	4	AAU00219	0219
19	430.5	42.	237	ψı	ABG78480	480 Wild
20		42.	233	4.	AAB73303	303
21	428.5	42.	233	7	ADE62921	921 Rat
22		42.	233	7	4	91 Rat P:
23		42.	233	N	æ	887
24	427.5	4 2	233	N	AAW05821	21 Bcl-XI
25		42.	233	N	53	30 Human a

45	44	43	42	41						ហ	3. <u>4</u>	ω u	3 2	31	30	29	28	27	8
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239	239	239	239	239	239	236	236	152	239	233	225	348	236	233	233	233	233	233	233
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AAU76553	ABG78478	ABG78479	AAB74127	AAB35130	AAW87810	AAU76554	AAB35131	AAG79760	AAG64037	AAB73304	AAW19396	ABR83557	ABR83558	ADE62493	AAB47515	AAG64262	AAB50538	AAY83223	AAY69969
6553	Abg78478	φ		0		4				Aab73304						262	α	3223	ω
Human Bcl	A human B	Murine Bc		Bcl-XL. 4	Human Bcl	Mutant ra	"DeprenyL	TolA-BCL	TOLA-BCL	Human Pro	Protein e	Human Bcl	Human Bcl		Human Bcl				

ALIGNMENTS

RESULT 1
AAY05531
ID AAY0 **222222** Spermatogenesis, Bcl-3; Bcl-2; mouse; fertility; infertility; animal model. 25-MAR-1999 Mus sp. Mouse Bcl-w protein essential for spermatogenesis 05-JUL-1999 AAY05531; AAY05531 standard; protein; 193 16-SEP-1997; 16-SEP-1998; WO9913710-A1 (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. (first entry) 97AU-00009228 98WO-AU000764. B 'ব --

Cory S, Adams J, Print C, Gibson L, Koentgen

N-PSDB; AAX25133. WPI; 1999-243890/20.

An animal model exhibiting reduced levels protein associated with Bcl-w. of a Bcl-w protein and/or

Claim 2; Page 35; 52pp; English.

sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic

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Best Local Sim.
Matches 193;
                             in the cell death pathway. The bol-2 family have both apoptotic act and the apoptosis blocking activity, bol-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo antisense constructs can be used in disorders where prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               facilitating
                                                                                                                                                       Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g.
                                                                                                                                                                                                                                                                                                                                                                                bcl-y;
                                                                                                                                                                                                                                                                                                                                                                                                      Rat bcl-y protein.
Sequence
                                                                                                 The mammalian bcl-y protein is a member of the bcl-2 family,
                                                                                                                       Example; Fig 3A; 27pp; English
                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                   WPI; 1998-446079/38
                                                                                                                                                                                                                         Guastella J;
                                                                                                                                                                                                                                                                     23-FEB-1996;
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                        desired
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                                                                                                                                                                                                                                                                                                                                                                                  pathway; apoptotic;
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Pred. No. 7
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7.4e-102;
                                                                                                                                                                                                                                                                                                                                                                                  apoptosis;
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Query Match Best Local Similarity

99.6%;

Score 1005; DB 2; Pred. No. 2e-101;

Length 193;

The present sequence represents rat bcl-y protein (Rbcl-y). The specification also describes human bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzhelmer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended

Disclosure; Col 15-18; 26pp; English

Novel bcl-y homologues of the rat and human bcl-2 protein - useful

for

N-PSDB; AAX15945

WPI; 1999-214150/18.

modulating

programmed

cell death.

Guastella

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RESULT 3
AAW97391
ID AAW9
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                                                                                                                                                                                                                                                                                                                                                                                      aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasi
                                                                                                                                                                                                                                                                         23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The rat bcl-y
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                                                                                                                                                                                                                                                                                                       25-NOV-1997;
                                                                                                                                                                                                                                                                                                                            16-MAR-1999
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97US-00798897.
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RESULT 4
AAW97393
ID AAW97393
AC AAW97399
XX AC AAW9
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AC AA
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Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat bol-y protein; Rbol-y; human bol-y protein; Hbol-y; bol-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma, Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; agging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis) Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 193 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein sequence of the specification.
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                                                                                                                                                Disclosure; Col 19-20; 26pp; English.
                                                                                                                                                                                                           modulating
                                                                                                                                                                                                                                   Novel bcl-y homologues of the rat and
                                                                                                                                                                                                                                                                                              WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1997;
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97US-00798897.
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Pred. No. 2e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 192 AA;
                                                                                          WPI; 1999-243890/20.
N-PSDB; AAX25132.
                                                                                                                                                                                                                                                                                                                        Spermatogenesis; animal model.
                                                                                                                                                                                                                                                                                                                                                               Human Bcl-w protein essential
                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY05530;
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                                                                                                                                                                                      16-SEP-1997;
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                                                                                                                                                                                                                                          25-MAR-1999
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                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 193
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Pred. No. 7.1e-101;
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                                                                                                                                                                                                                                                                                                                                        human;
                                                                                                                                                                                                                                                                                                                                                                  spermatogenesis.
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                                                                                                                                                                                                                                                                                                                                        fertility; infertility;
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The present sequence is

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Bc1-2

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An animal model exhibiting reduced protein associated with Bcl-w.

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RESULT 6
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Best Local Similarity
Matches 191; Conserv
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                                                                                                                                                                                                                                                                                                                                                    14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic cons spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Protein Q92843,
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                                                                                                        GENBANK; Q92843
                                                                                                                                      WPI; 2003-268312/26.
                                                                                                                                                                                                       Woolf
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                                                                                                                                                                                                                                                           (GEHO ) GEN HOSPITAL (FARB ) BAYER AG.
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                                                                                                                                                                                                 D'urso
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                                                                                                                                                                                                       Befort
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         injury, chronic constriction injury, CCI, NI; Chung.
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Pred. No. 7.1e-101;
1; Mismatches 1;
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The invention discloses a composition comprising two or more isolated rat cor human polymucleotides or a polymucleotide which represents a fragment, contributive or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the mucleic acid sequence contributive or allelic variation of the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a cit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal compound that is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polymucleotide sequence which is differentially compound that regulates the activity of one or more of the specification, a method for identifying a compound which regulates the activity in an animal of one or more of the polymucleotides, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polympetides or their antibodies. The polymucleotide or the compound that regulates the activity in an animal of one or more of the polympetides or their antibodies. The polympetides or the compound that polympetides or their antibodies. The polympetide or the compound that injury (CCI) and spared nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (Chung), chronic constriction the sequence data for this patent did not form part of the printed conspective twoshes, introbubrinhished soft semimeres.
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Sequence
                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
     193
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                                                                                                                                                                                       Local Similarity hes 191; Conserv
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181
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                                                                                                                                                         QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                      GALVTVGAFFASK 193
                                             QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                              <u>MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT</u>
                                                                                             FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
GALVIVGAFFASK 193
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                     99.18;
                                                                                                                                                                                          1.
                                                                                                                                                                                         Score 1000; DB 7;
Pred. No. 7.1e-101;
1; Mismatches 1;
                                                                                                                                                                                                                 Length 193;
                                                                                                                                                                                            Indels
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RESULT 7
AAW61392
AAW61392 standard; protein; 193
              04-AUG-1998
                                                        bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis;
                                                                       Human bcl-y protein.
                                                                                     02-OCT-1998
                                                                                                    AAW61392;
11-FEB-1997;
                            US5789201-A.
                                           Homo sapiens
                                                                                     (first entry)
97US-00798897
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New composition comprising preparing a medicament for

two or more isolated polypeptides, useful for treating pain in an animal.

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RESULT 8
AAW97
AAW97
AAW
XX AAW9
XX AAW9
XX The
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XX Rat
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The mammalian bcl-y protein is a member of the bcl-2 family, componed in the cell death pathway. The bcl-2 family have both apoptotic act and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo.
                                                                                                                                                                                                                                                         Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardia infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding B-cell lymphoma-y protein - useful recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guastella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisense constructs can be used in disorders where prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Column 17/18; 27pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97392 standard; protein; 193
                                                              16-MAR-1999
                                                                                                                      US5883229-A.
                                                                                                                                                                              Homo
                                                                                                                                                                                                                                 Kaposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-446079/38
DB; AAV28334.
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                                                                                                                                                                                                                                 lung cancer; autoimmune; hyperimmune disease; parasite
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Pred. No. 2.5e-100;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                  stroke;
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190;

Conservative

1;

Indels

0;

Gaps

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The present sequence represents human bcl-y protein (Hbcl-y). The CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-CY are homologues of the bcl-2 protein thought to be involved in CC proteins may be used to treat conditions associated with a disruption of CC the cell death pathway. If they act as cell death inhibitors, they may be CC used in therapies to treat subjects suffering from: strokes, head trauma, CC Alzheimer's Disease, neural and muscular degenerative diseases CC (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis CC -conditions where cells under go premature cell death as a result of CC conditions where cells under go premature cell death as a result of CC way to develop cell lines which remain viable in culture for an extended CC period. In contrast, if they act as cell death stimulators, Rbcl-y and CC the span such as cancer (especially kaposi's sarcoma and lung cancer) CC and auto/hyperimmune diseases. They may also be used to cause cell death CC in, and hence control, parasites
Query Match
Best Local S
Matches 190
                                                                        Sequence 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulating programmed cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel bcl-y homologues of the rat and human bcl-2 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX15946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-214150/18
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11-FEB-1997;
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                   Similarity
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                                                                            AA;
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97US-00798897.
                 98.6%;
 Score 995; DB 2; I
Pred. No. 2.5e-100;
1; Mismatches 2;
                                     Length 193;
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RESULT 9
AAW36047
ID AAW3
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AC AAW3
AC AAW3
AC BC1-
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DT 22-A
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DT 22-A
XX
DT 4149
CE Huma
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                                                                                                                                                                                                                                                                                                                                                                           FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                            GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                      GALVIVGAFFASK 193
                                                                                                                                                                                                                                                                                                   QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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25-NOV-1997;

97US-00978523

Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease.

Human bcl-w protein.

AAW36047;

22-APR-1998

(first entry)

AAW36047 standard; protein;

193

Homo sapiens

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RESULT 10
AAY05532
ID AAY05532
AC AAY05
XX AAY05
XX O5-JU
DT 05-JU
DX Human
XX Sperm
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Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a novel human protein, bol-w, encoded by the bol 2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bol-w for therapy, diagnosis, antibody production or screening of potential modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding apoptosis related gene bcl-w - used to induce inhibit cell survival, e.g. for treatment of cancer and degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cory S,
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                                                                                      Spermatogenesis; animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 48; 86pp; English
                                                                                                                                      Human Bcl-w protein essential
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DB; AAT96577.
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                                                                                                                                                                                                                                      standard;
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                                                                                                       Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                    protein;
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                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.4%;
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Pred. No. 4.2e-100
2; Mismatches 2
                                                                                                                                      for spermatogenesis
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                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An animal model exhibiting reduced levels of a protein associated with Bcl-w.
                                                                                                                                                                                                                                                                                                                    Sequence 193 AA;
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                                                                                                                                                                                                                                                                                                                                                       can induce infertility
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                                                                                                                                               FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
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                            GALVIVGAFFASK 193
GALVIVGAFFASK 193
                                                             QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                             PSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                         98.4%;
ilarity 97.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52pp; English.
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Pred. No. 4.2e-100;
2; Mismatches 2;
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RESULT 11
AAW97394
AAW97394 standard; protein; 192
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Mammalian bcl-y protein.

20-MAY-1999

(first entry

ZZZZZZZZZZZZZZZ Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; stroke;

WO9913710-A1

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AAY05533
ID AAY0
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AC AAY0
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DT 05-0
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                                                                                                                                                                                                                                                                                                                                                                                                 CC The present sequence represents a mammalian bcy-l protein. The CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein CC thought to be involved in programmed cell death (apoptosis and necrosis). CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated cc with a disruption of the cell death pathway. If they act as cell death CC inhibitors, they may be used in therapies to treat subjects suffering CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular CC degenerative diseases (especially multiple sclerosis), myocardial cc infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel bcl-y homologues of the rat and modulating programmed cell death.
 05-JUL-1999
                           AAY05533
                                                 AAY05533 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Col 19-22; 26pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1996;
11-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                      ALVTVGAFFASK 193
                                                                                                                                                                                            VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
                                                                                                                                                                                                                                                                                            ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF
                                                                                                                                                                                                                                                                                                                                                                              192 AA;
                                                                                                                                                                    VOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG
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                                                                                                                                                                                                                                                                         ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF
                                                                                                                   ALVIVGAFFASK 192
                                                                                                                                                                                                                     SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ
                                                                                                                                                                                                                                                                                                                            Conservative
 (first entry)
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97US-00798897.
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AAW36048
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Matches 185;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is described of a derivative of mouse Bcl-w (see also AAY05531), a pro-survival member of the Bcl-2 family that is widd expressed and which is essential for spermatogenesis. The derivative lacks the 24 N-terminal amino acids of Bcl-w. The invention relates generally to a method of treatment and to an animal model for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility; animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enhancing or otherwise facilitating spermatogenesis in animals, or which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 39; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An animal model exhibiting reduced levels protein associated with Bcl-w.
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                                                 GALVIVGAFFASK 193
                                                                                                QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL
                                                                                                                                               QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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GALVIVGAFFASK 192
                                                                                                                                                                                                    FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 967.5; DB 2
Pred. No. 2.5e-97;
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AAW36048

AAW36048 standard; protein; 168

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RESULT 14
AAO18223
ID AAO18
XX AAO18
XX AAO18
XX IS AC AAO18
XX IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding apoptosis related gene inhibit cell survival, e.g. for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1996;
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diagnosis; degenerative disease.
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                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MATEASTEDTRALVADEVGYKLROKGYVCGAGEGEGEAADELHOAMRAAGDEFETRERRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams
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                                                                                                                                                                                                                                                                                                                                                     QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA
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                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATIONS PTY LTD.
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97.0%;
                                                       domain
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Pred. No. 2.2e-87;
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Human;

apoptotic signal transduction

protein; Bcl-Rambo; BHNo domain;

RESULT 15
AAW59884
ID AAW59
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AC AAW59
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DT 20-NC
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Amino
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BC1-1
KW immun

20-NOV-1998 AAW59884;

(first

0£ entry)

the CDNA

clone Bcl-like

(HAICH29)

AAW59884 standard;

protein;

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Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.

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Best Local :
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                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of the human Bcl-Rambo apoptotic transcription factor, particularly the BHNo domain. The sequences are useful in the treatment of diseases caused by incorrectly regulated intracellular signal transduction, including cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's diseases), muscular dystrophy, viral infections (including human immunodeficiency virus), autoimmune disease, septic shock, graft versus host disease and acute hepatitis. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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immunosuppressive; anti-HIV; antibacterial; hepatotropic; septi
Parkinson's disease; muscular dystrophy; HIV; viral infection;
                                                                                                                                                                                                                                                                                                                        Sequence 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-2000; 2000DE-01061766.
04-JAN-2001; 2001DE-01000280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;
nootropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory;
immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 61pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-2001; 2001WO-EP014597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors identifying therapeutic modulators of Bcl-Rambo function.
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                                                                                         QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                   MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                           FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                            MATPASAPXTXAXVAD-XGYKLRQKGYVNGAGPGXGPAAD-XHQAXRAAGXEFETRFXRT
 GALVTVGAFFASK 190
                             GALVTVGAFFASK 193
                                                              QXQEXMVAYLETXLAX-IHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                             FSDLAAQLHVTPGSAQQRFTQVSDELFQGXPNWGXXXAFFVFGAAXCAESVNXEMEPLVG
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                                                                                                                                                                                                                                                                        80.7%;
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Pred. :
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No. 1.4e-80;
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                                                                                                                                                                                                                                                                                        Length 190;
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Best Local Similarity 98.6%;
Matches 142; Conservative 1
                                                                                                                                                                                                                                                        This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis
                                                                                                                                                                                                                                   Sequence 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies or tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-414099/35.
N-PSDB; AAV41925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ni J, Rosen CA, Gentz RL,
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21-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC. (AUCK-) AUCKLAND UNISERVICES LTD.
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                                                                                                                                 1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                QVQDWMVAYLETRLADWIHSSGGW 144
                                                                       FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                        FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                  MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
 QVQEWMVAYLETRLADWIHSSGGW 144
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97US-0034205P.
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Search completed: March 25, Job time : 52 secs

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